

FIGURE 1A

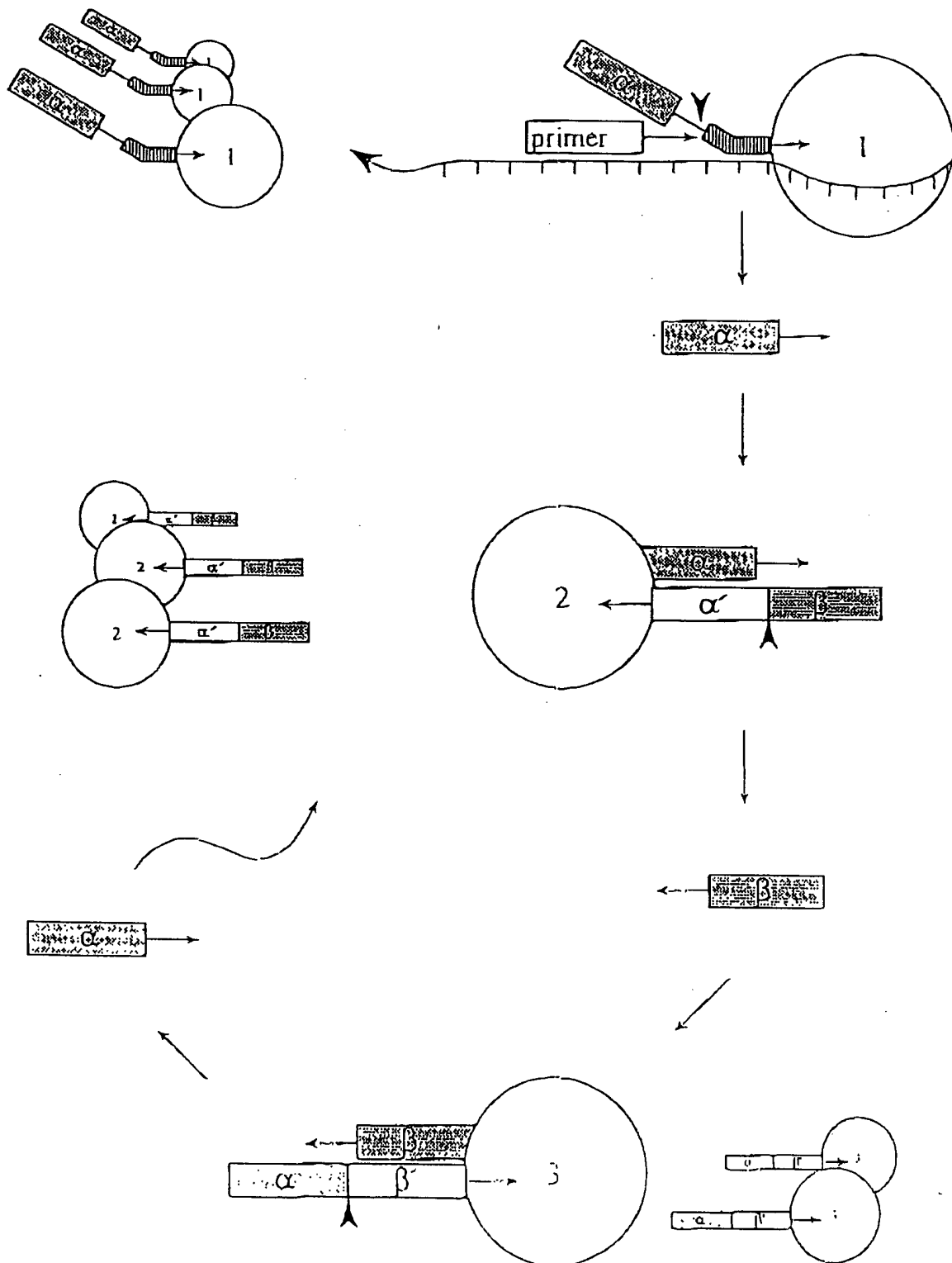
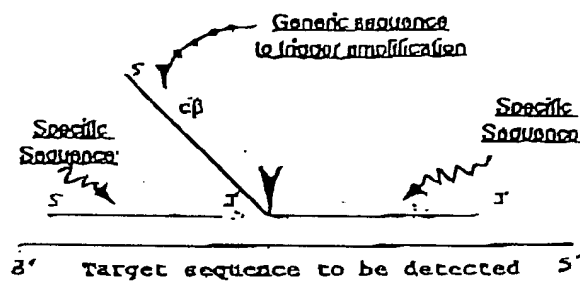


FIGURE 1B

## PART ONE: TRIGGER REACTION



## PART TWO: DETECTION REACTION

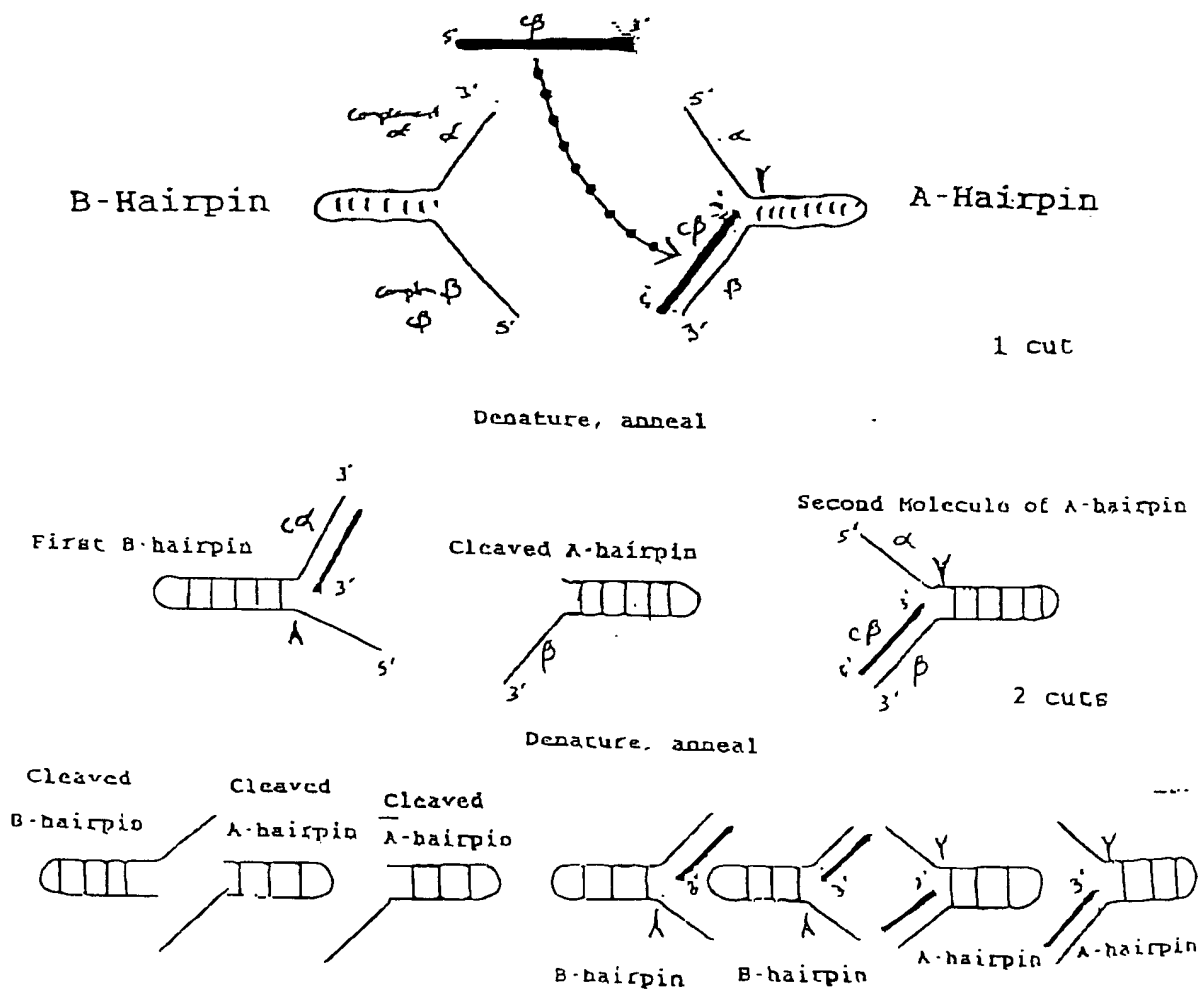




FIGURE 2 (con'd)

MAJORITY (SEQ ID NO:7)	CCACCCCGACGACCTXCTCCCCACCCCTGCCCAAGAGCGCGGAAAGGAGGGGTACGAGGTCCGGCATCCCTC	
DNAPTAAO (SEQ ID NO:1)	.....C.....G.....C.....C.....	417
DNAPTFL (SEQ ID NO:2)	I.....G.....CG.....	414
DNAPTHH (SEQ ID NO:3)	.....T..G.....	420
MAJORITY	ACCGCCGACCGCGGACCTCTACGAGCCTCTTCCGACCGGATCGGGCTCCCTCCACCCCGAGGGGTACCTCA	
DNAPTAAO	.....AAA.....T.....CA.....	487
DNAPTFL	.....T.....G.....G.....A.....T.....G.....	484
DNAPTHH	.....A..G..G.....G.....CC.....	490
MAJORITY	TCACCCCGCGCGCTTCCGAGAACTACCGCCCTGACCGCCGAGCACTGGGTGGACTACCGGCGCGCTCGG	
DNAPTAAO	.....C.....A.....C.....C.....CC.....A.....	557
DNAPTFL	.....AC.....C.....C.....	554
DNAPTHH	.....A.....C.....C.....T..C.....C..T..	560
MAJORITY	CGCGGACCCCTCCGACAACTCCCGCGGGTCAADGGCATCCGGGGAAGAGCCCGCCXCAAGCTCCCTCXAG	
DNAPTAAO	.....GAG.....T.....G.....G.....T..CG.....	627
DNAPTFL	.....G..I..A.....G.....A..G.....A..CGG	624
DNAPTHH	.....T.....TC.....A.....	630
MAJORITY	GAGTCGGCGGACCGCTCGAAACCTCTCAAGAACCTCGACCGCGGTCAACCCCGC...CXTCGGCGGACAGAGA	
DNAPTAAO	.....CG.....G.....C.....A.....	694
DNAPTFL	.....I..C..C.....A.....T..T..G.....C	691
DNAPTHH	.....A.....A.....A.AAA..C.....	700

4

FIGURE 2 (cont'd)

[illegible]

FIGURE 2 (cont'd)

MAJORITY	(SEQ ID NO:7)	CCCCCXCTCCTCCGCAACGACCTGGCCGCTTTCGCCCTCAGCGAGCCGCCCTCXTCGCCCGCGGACG	
ONAPTAO	(SEQ ID NO:1)	.....C..T.....A.....AC.....C.....A.....T..C.....CC.....C.....	1111
ONAPTR	(SEQ ID NO:2)	.....AA.....C.....G.....C.....C.....T..C..A..A.....	1120
ONAPTH	(SEQ ID NO:3)	.....C.....C.....C.....C.....TC.....G..A.....G.....	
MAJORITY		ACCCCATGCTGCTGGCTAGCTGCTGGACCCCTCCACACGACCCCGGAGCGGGGTGGCCCGCGGCTACGG	
ONAPTAO		.....T.....	1184
ONAPTR		.....T.....	1181
ONAPTH		.....T.....	1190
MAJORITY		CGCCGAGTCCAGCGGACGAXCGCGGGGAGCGCGGCTCGTXXTCGAGAGGCTCTTCXGAAAGCTXXXGGAG	
ONAPTAO		.....G.....G.....GC.....T.....GC.....G.....G.....G.....G.....	1254
ONAPTR		.....T.....A.....G.....GC.....C..G.....A..G.....AAA.....	1251
ONAPTH		.....C..C..CGC..G.....C..G.....CAT..G.....CGTA.....	1260
MAJORITY		CGCCCTTGCAGCGGAGCGAGCGCTGCTTGGCTTTACCGAGGAGCTCGAGAACCGCCCTTTCGCCCGGCTCGCTCG	
ONAPTAO		A..G.....A.....A..A..AC..C..G.....G.....G.....GCT.....	1324
ONAPTR		.....C.....A.....C.....C.....C.....G.....G.....G.....GCT.....	1321
ONAPTH		.....C.....A.....C.....C.....C.....A.....C.....G.....	1330
MAJORITY		CCACACATGGAGGCGCGGCGGIXCGGCTCGACGTCGCGCTAGCTCGAGCGGCGCTXTCGCTGGAGCTGGCGGA	
ONAPTAO		.....G.....G.....C.....T.....AG.....T..G.....C.....	1394
ONAPTR		.....G.....C.....C.....C.....C.....C.....A..C.....	1391
ONAPTH		.....C.....A.....C.....C.....T.....T.....C..I.....	1400

FIGURE 2 (cont'd)

MAJORITY	(SEQ ID NO:7)	GGAGATCCCGCGGCTCGAGGAAAGGCTCTCCGGCTCGCGCGGCAACCGCTCAACCTCCCGGGAC	
ONADTAD	(SEQ ID NO:1)	.....GC.....GC.....	1464
ONADTRL	(SEQ ID NO:2)	.....G.C.....AC..G.....	1461
ONADPTH	(SEQ ID NO:3)	.....T.....C.....	1466
MAJORITY		CAGC1CGAARAGGCTGC1CTT1GACGAGGCTXGCGGCTTCGCGCGCATCGGCAAGCGGAGAGACXCGGCAAGC	
ONADTAD		.....G.....A.....	1534
ONADTRL		.....GC.....G.C.....C..G..T.....	1531
ONADPTH		.....TA.....T.G..G.....C.A.....	1540
MAJORITY		GCTCCACGAGCGCGCGCTGCTGCAGCGGCTXCGXGAGCGCGGCAACCGCATCGTGGAGAAAGATCCTCCAG1A	
ONADTAD		.....C.....C..G.....	1604
ONADTRL		.....T.....G.A.....	1601
ONADPTH		.....G.....A.G.....	1610
MAJORITY		CGCGGAGGTCACCAAGGTCAGAGAAACGCTACATXGACGCGGCTGCGXGCGCTGCTCCACCGCGGACGCGGC	
ONADTAD		.....G.....G.....T.....C.A.....A.....	1617
ONADTRL		.....A.....A.....C.C.....C.....	1621
ONADPTH		.....G.C.....C.AAG.....G.....	1680
MAJORITY		CCCC1CCACACCGCGCT1CAACCCACACCGCGCCACCGCGCGCGCGCT1AGTAGCTCCGACCGCCCAACCTCC	
ONADTAD		.....A.....A.....T.....	1744
ONADTRL		.....G.....C.....TCC.....	1741
ONADPTH		.....G.....G.....	1750

7

FIGURE 2 (cont'd)

MAJORITY (SEQ ID NO:7)	AGAACATCCCGCCTCCGACCCXCTGGCCACAGCAATCCGCCCGGCTTCCTGGCCGAGGAGGCTCCGT	
DNAPTAD (SEQ ID NO:1)	.....G..T..G.....A..C.....C...C..	1814
DNAPTR (SEQ ID NO:2)	.....G.....T.....C..C.....A.....C.....C.....	1811
DNAPTH (SEQ ID NO:3)	.....CT.....T.....C.....C.....T.....C.....	182
MAJORITY	CTTCTGGCCCTCCACTATAGCCAGATAGAGCTCCGGTCTTGGCCGACCTCTCCGGGAGGAGAACCTG	
DNAPTAD	A.....T.....T.....A.....G.....C.....	1894
DNAPTR	.....T..T.....C.....T.....T.....C.....	1881
DNAPTH	.....T.....C.....C.....C.....A.....	1890
MAJORITY	ATCCGGCTCTCCAGGAGCGGAGGACATCCACAGCCGACAGCGCCAGCTGGATGTTCCGGCTCCGCCCGG	
DNAPTAD	.....G.....G.....G.....G.....G.....	1954
DNAPTR	.....T.....T.....T.....T.....T.....	1951
DNAPTH	.....A.....A.....A.....A.....A.....	1960
MAJORITY	ACGCCCTCCACCCCTGATGCCCGCGCGCGCGCCAGACCAATTCGGCGCTCTACGCCCACTGTCGG	
DNAPTAD	.....A..GG...A.....T.....GG..G.....C.....	202
DNAPTR	.....A..GG...A.....T.....GG..G.....C.....	2021
DNAPTH	.....A..GG...A.....T.....GG..G.....C.....	2030
MAJORITY	CCACCCCTCTCCAGGAGCTTCCCATCCCTACGAGGAGCGCGCTGGCTTCATTCAGCCCTACTTCAG	
DNAPTAD	.....A.....T.....T.....CCA.....T.....	2094
DNAPTR	.....GG.....T.....T.....T.....T.....	2091
DNAPTH	.....TA..G.....T.....T.....T.....A.....	2100



FIGURE 2 (cont'd)

MAJORITY (SEQ ID NO:7)	AGCTTCCCCCAAGCTCCGGCCCTCCATTCAGAAACACCCCTCCAGGAGCCCAAGCCGGGGCTACCTCCAGA	2184
ONAPTAO (SEQ ID NO:1)	.....	2184
ONAPTR (SEQ ID NO:2)	.....	2184
ONAPTH (SEQ ID NO:3)	.....	2177
MAJORITY	CCCTCTTCCCGCCCGCCCTACCTCCCGGAGCTCAACGCCCGCTCAAGAGGCTCCCGGAGCCCGCCCA	
ONAPTAO	.....	2234
ONAPTR	.....	2231
ONAPTH	.....	2240
MAJORITY	CGCCATCGCCCTTCAACATCGCCGCTCCAGCGCCAGCCCGCCGACCTCATCAAGCTGCCCATCGTCAAGGCTC	
ONAPTAO	.....	2304
ONAPTR	.....	2301
ONAPTH	.....	2310
MAJORITY	TTCCCGCCGCTXCAGGAAATCGCGCCAGGATGCTCCIXCAGGICCAAGCAGCCTCGTCCCTCCAGGCCC	
ONAPTAO	.....	2371
ONAPTR	.....	2371
ONAPTH	.....	2380
MAJORITY	CCAAACACCGCGCCGAGCGTGGCCGCTTCCCGCAGGAGGCTCATCGAGGCGCTCTATCGCCCTCGCCCT	
ONAPTAO	.....	2444
ONAPTR	.....	2441
ONAPTH	.....	2450

FIGURE 2 (cont'd)

MAJORITY (SEQ ID NO:7)	CCCCCICGAGGICGAGGICGCGGATCGCGGCAAGGACTCGGICCTCCCCCAAGGAGIAC	2499
CHAPTAD (SEQ ID NO:1)	.....A.....CA	2496
CHAPTR (SEQ ID NO:2)	.....CC.....	2505
CHAPTH (SEQ ID NO:3)	.....[.....07...	

## FIGURE 3

MAJORITY (SEQ ID NO:8)	HXAWLP(LFEPKGRVLLVOGHHLAYRTFFALKQLTISRCEPVOAVYCFAKSLLKALKECC·DAVXVVFQAK	
TAQ PRO (SEQ ID NO:4)	AG.....H.....	9
TR PRO (SEQ ID NO:5)	.....V.....	
TTM PRO (SEQ ID NO:6)	E.....YK.....F.....	70
MAJORITY	APSFARAEAYEAYKACRAPTPEOPROLALIKELVDLLGLXALEVPGYEADOVLAFLAKXAEKECYEVRIL	
TAQ PRO	GG.....A.....S.....	139
TR PRO	.....V.....F.....A.....	138
TTM PRO	.....F.....	140
MAJORITY	TADRDLYQLLSDRIAVLHPEGYLIIPAWLWEKYGLRPEQWVDYRALXODPSDHLPGVKGICETAXKLLX	
TAQ PRO	K.....H.....D.....A.....Y.....E.....	209
TR PRO	.....E.....Y.....A.....	OR, IR 208
TTM PRO	V.....V.....H.....E.....F.....V.....	L...K 210
MAJORITY	EWGSLHLLKXLOAVKP·XXREKIXAHMEDLXLSXXLSXVATDLPLEVDFAHAREPDREGLEAFLEALF	
TAQ PRO	A.....L...AL...L...D...K...WO...AK...	278
TR PRO	FOH...O...SL...LO...G...A...A...AX...O...H...	277
TTM PRO	ENV...K...L...A...LE...A...L...OC...	280
MAJORITY	GSLLEFGLLXPKALCEAPWPPPEGAFVGFVLSAPEPMWAEELLALAAARXGAVHRAAXOPLXGLROLKXEV	
TAQ PRO	S.....K.....D.....C.....PE...YKA.....	A 348
TR PRO	G...A...L...SF...L...G...WE...L...Q...R...G...	347
TTM PRO	A...AP...K...C...D...A...A...A...K...	350

//

MAJORITY (SEQ ID NO:8)	SEQ ID NO:4	SEQ ID NO:5	SEQ ID NO:6
IAO PRO	IAO PRO	IAO PRO	IAO PRO
ITL PRO	ITL PRO	ITL PRO	ITL PRO
ITM PRO	ITM PRO	ITM PRO	ITM PRO
MAJORITY	MAJORITY	MAJORITY	MAJORITY
IAO PRO	IAO PRO	IAO PRO	IAO PRO
ITL PRO	ITL PRO	ITL PRO	ITL PRO
ITM PRO	ITM PRO	ITM PRO	ITM PRO
MAJORITY	MAJORITY	MAJORITY	MAJORITY
IAO PRO	IAO PRO	IAO PRO	IAO PRO
ITL PRO	ITL PRO	ITL PRO	ITL PRO
ITM PRO	ITM PRO	ITM PRO	ITM PRO

FIGURE 3 (cont'd)

MAJORITY (SEQ ID NO:8)	SFPKVRWIEKTL EECRRRCYVETL FORRRYVPDLNAAVKSVRAEAAERMAFNMPVQOOTAADLHKLAMVXL	
IAQ PR0 (SEQ ID NO:4)	.....	700
TL PR0 (SEQ ID NO:5)	Y.....	767
TH PR0 (SEQ ID NO:6)	.....K.....	770
MAJORITY	FPRLEXMGARMLOVHDELVL EAPKXRAEXVAAALAKENVHEGVYPLAVPLEVEVCGCEDWLSAKEX	
IAQ PR0	.....E.....	833
TL PR0	.....O.L.....	831
TH PR0	.....R.....	835

FIGURE 4

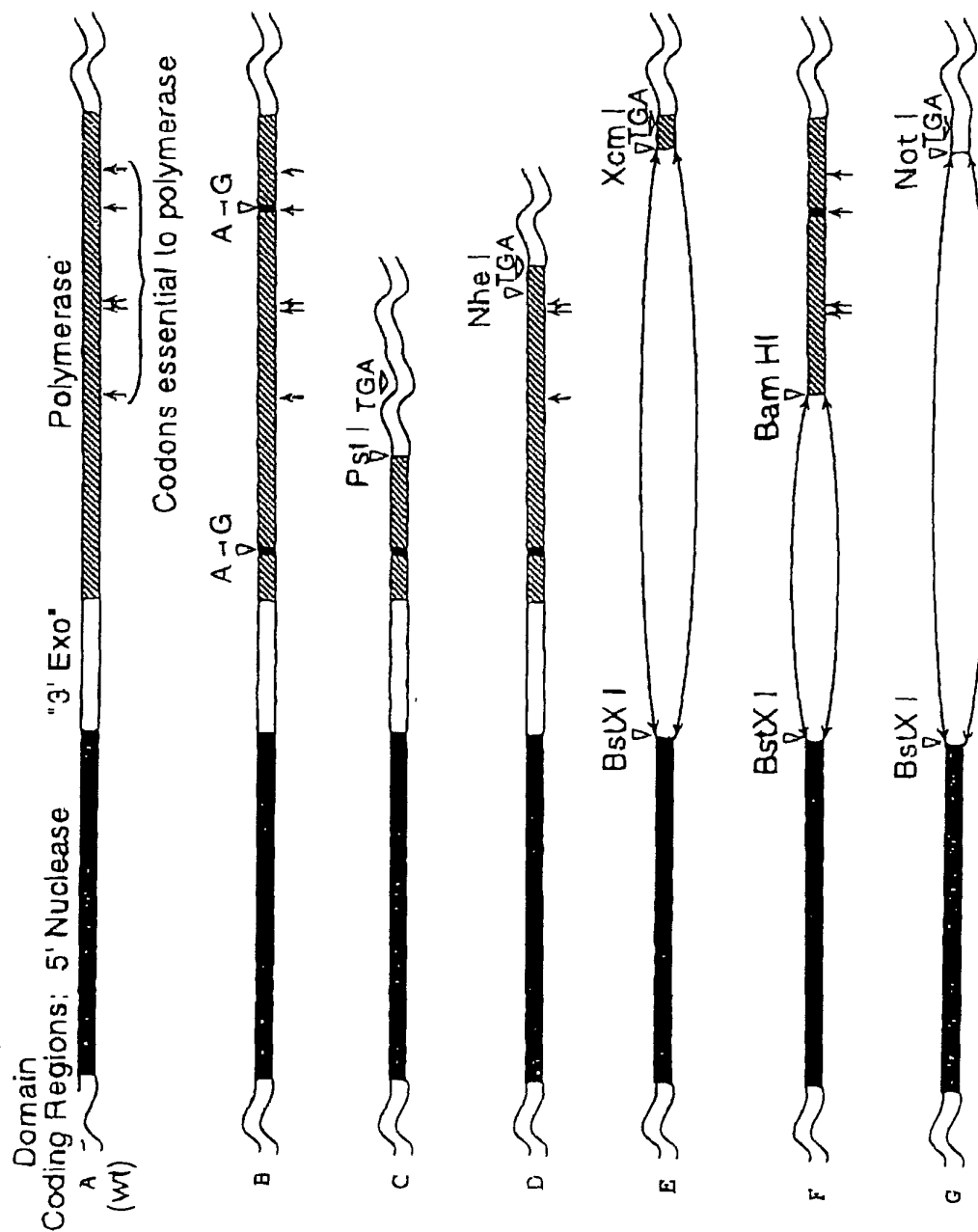


FIGURE 5

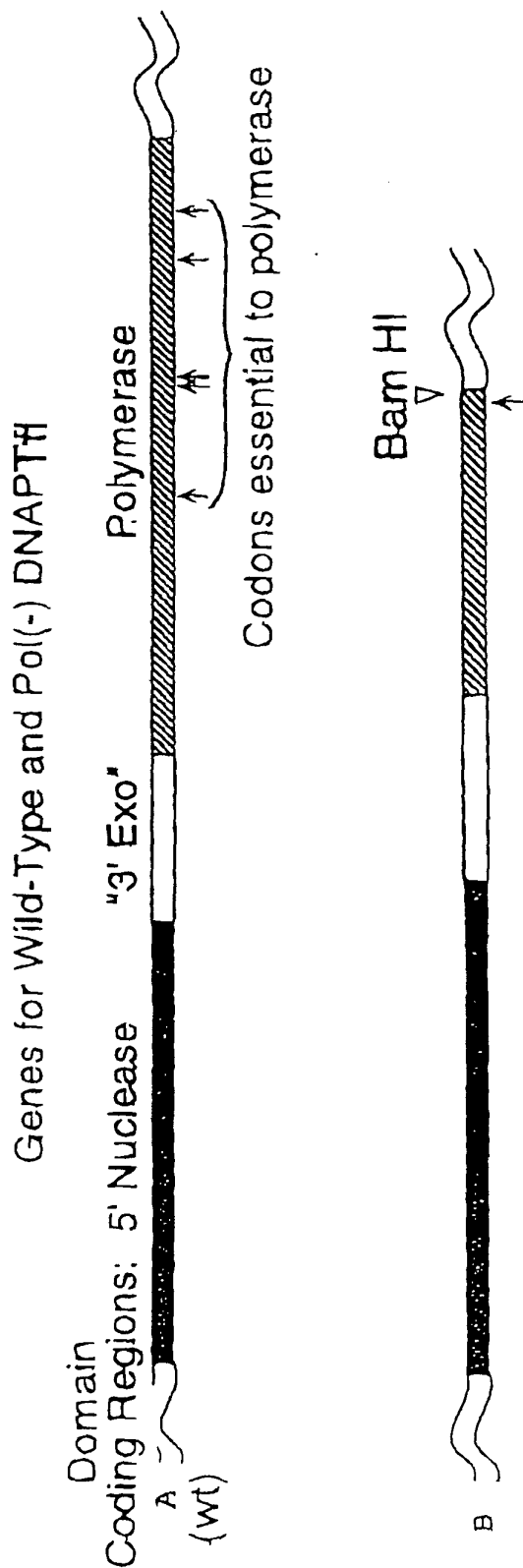


FIGURE 6

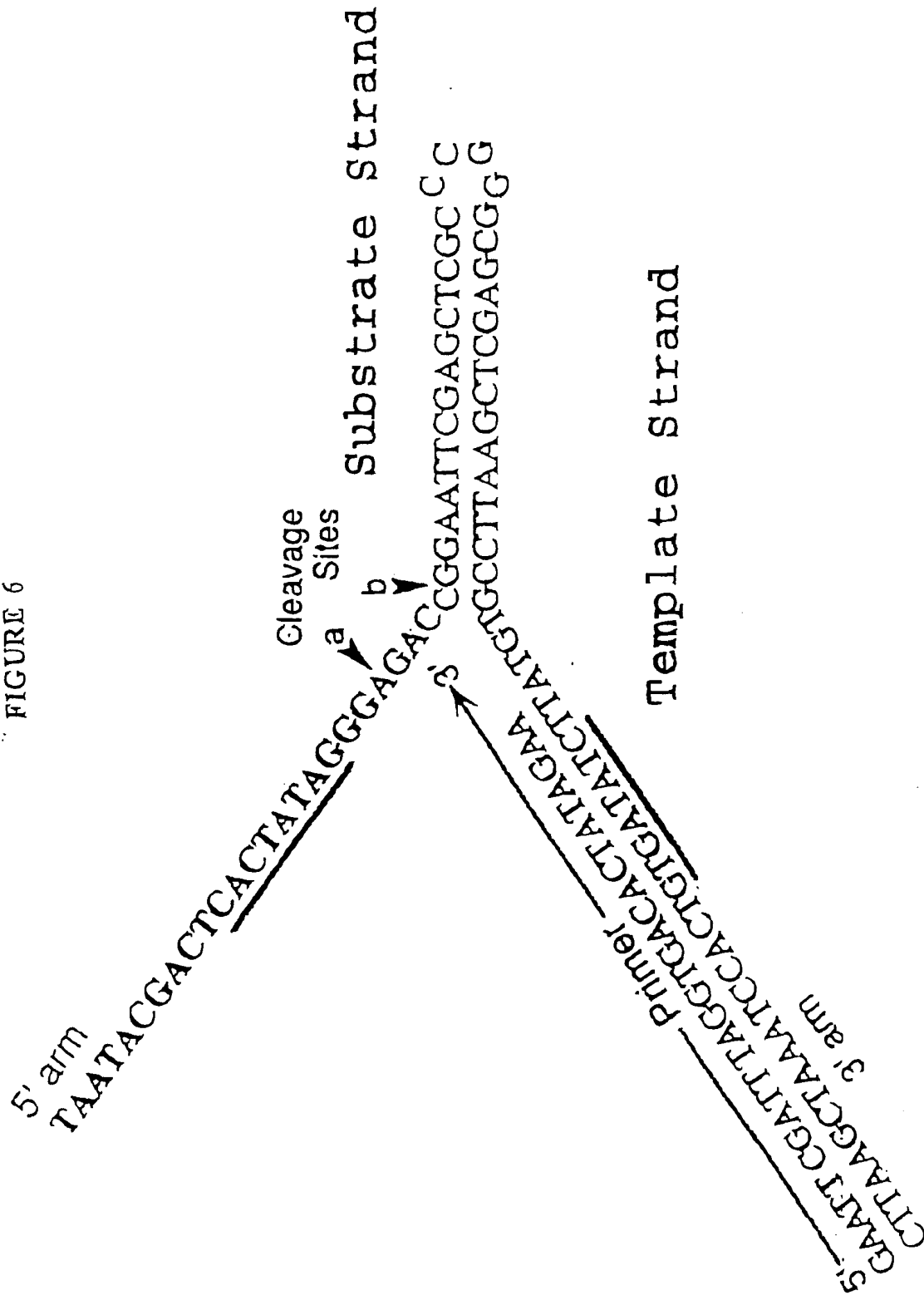




FIGURE 7

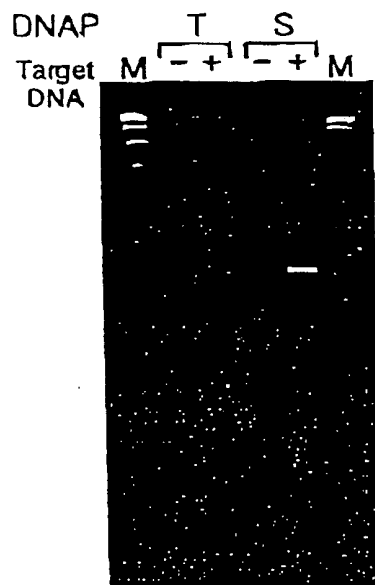


FIGURE 8

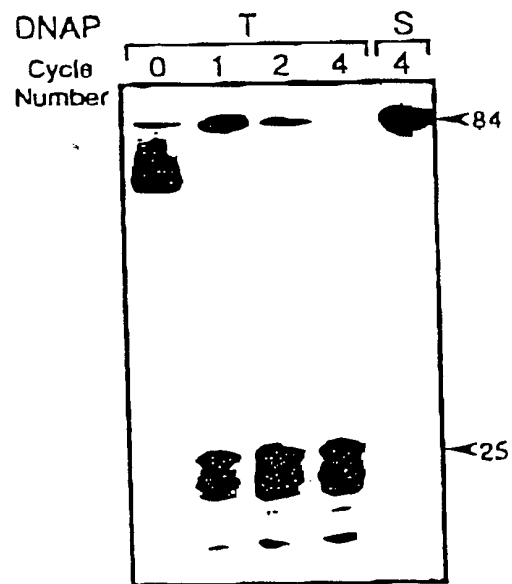


FIGURE 9

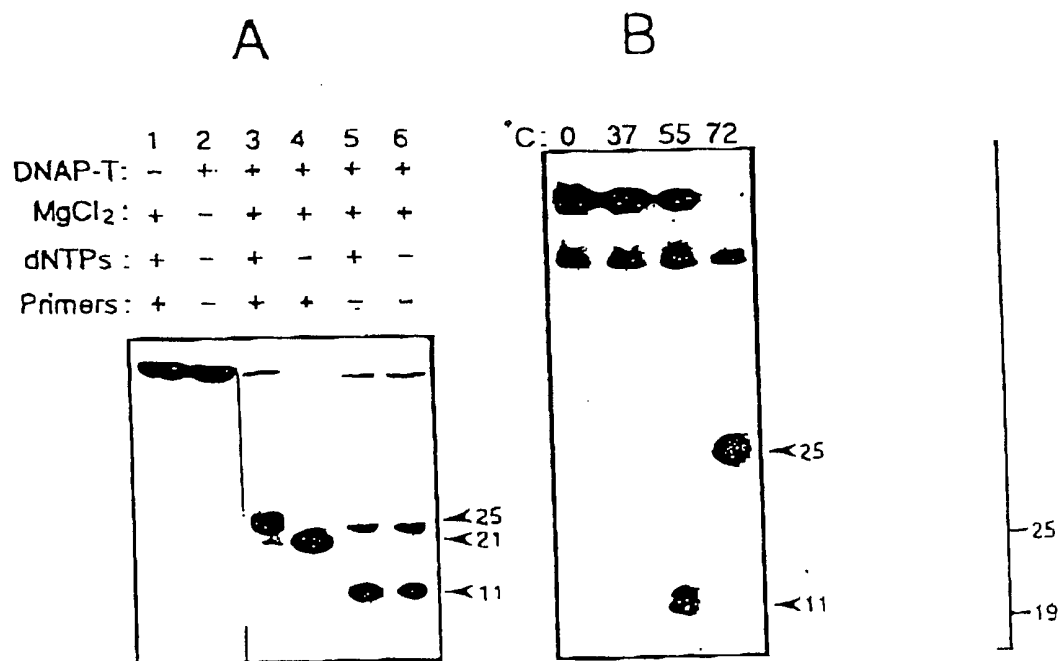


FIGURE 10

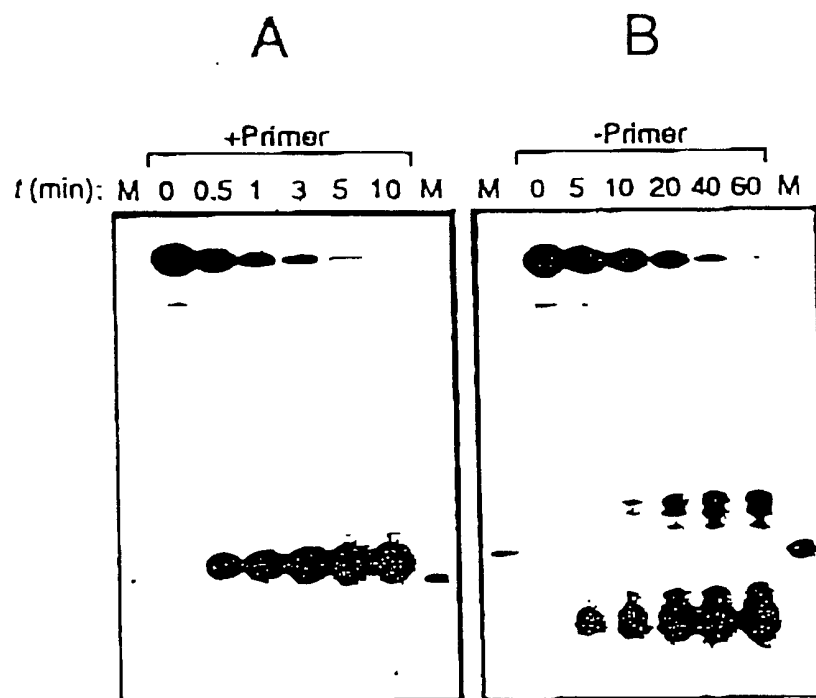


FIGURE 11



FIGURE 12

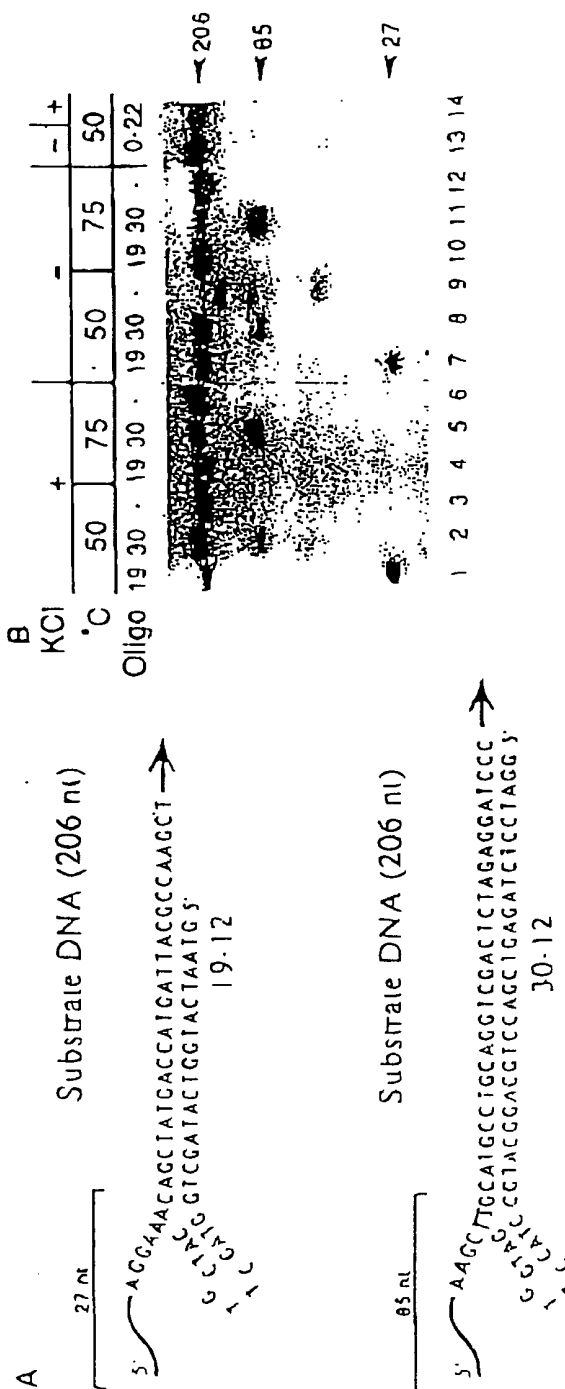


FIGURE 13

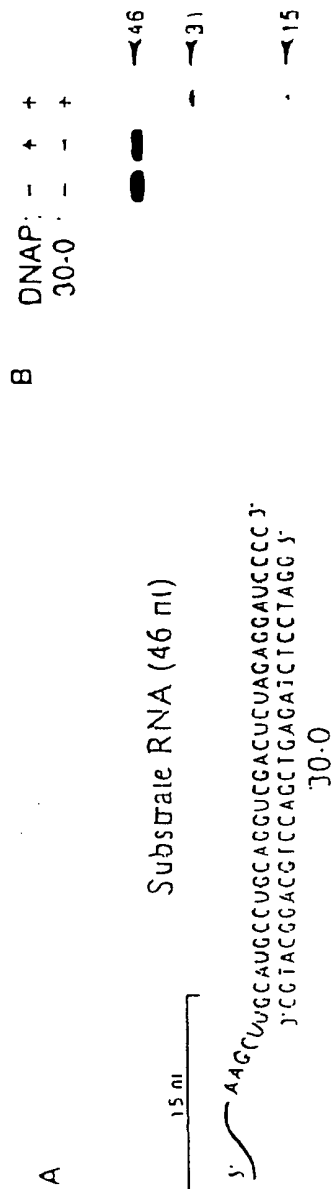


FIGURE 14

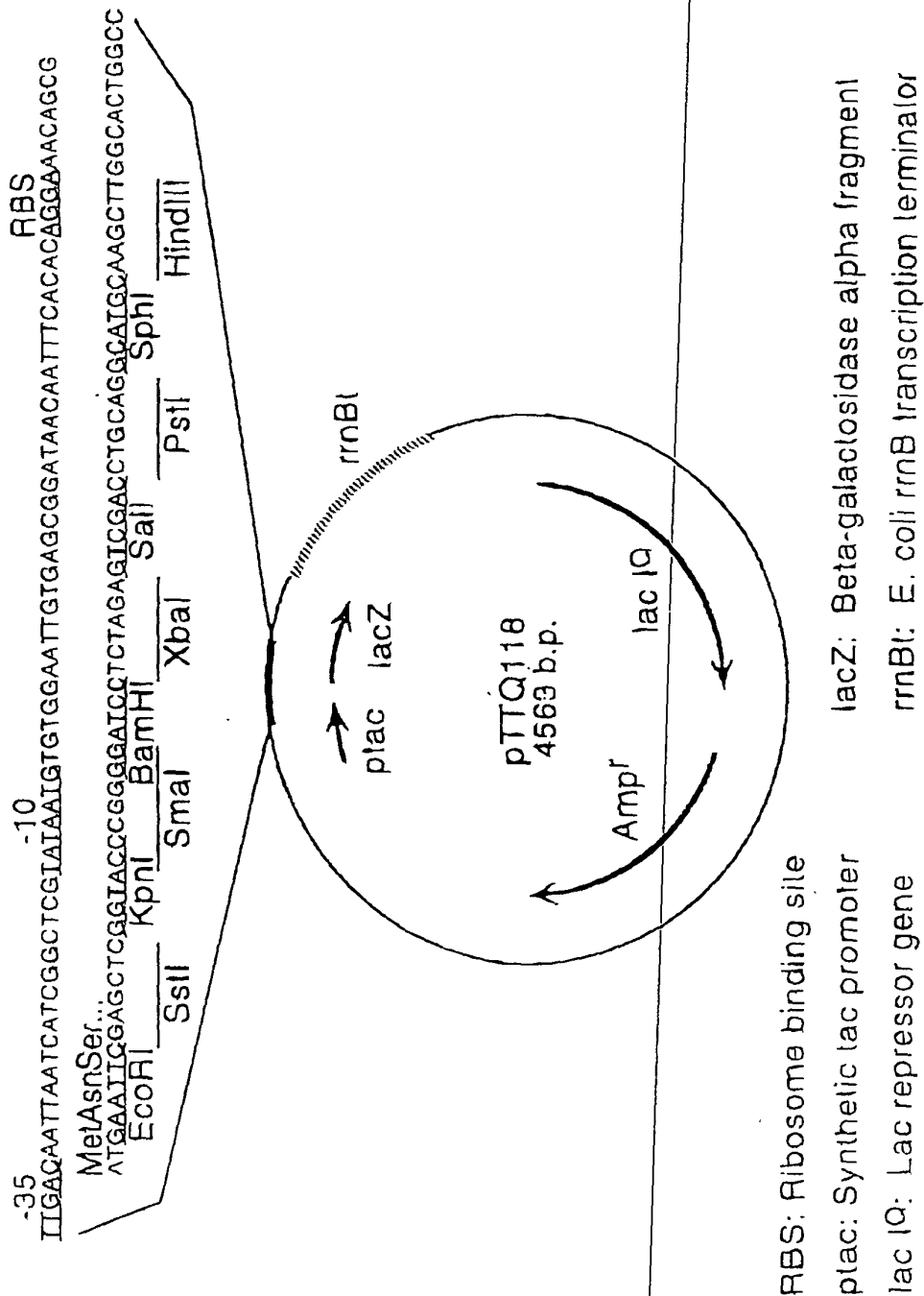
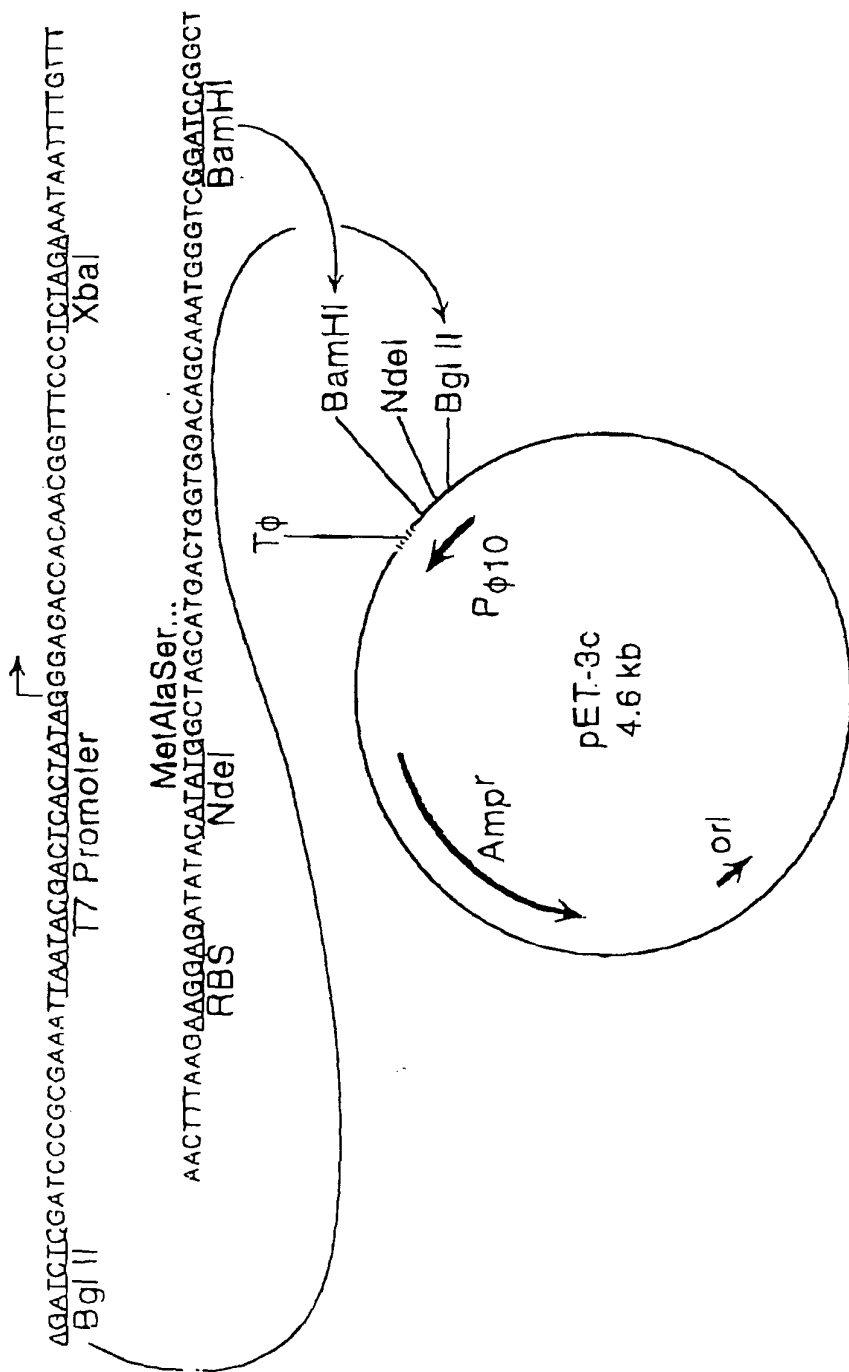




FIGURE 15



P<sub>φ10</sub>: Bacteriophage T7 φ10 promoter

T<sub>φ</sub>: T7 φ Terminator

RBS: Ribosome binding site



FIGURE 17

1 2 3 4 5 6 7

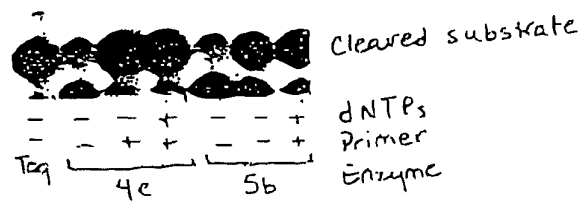
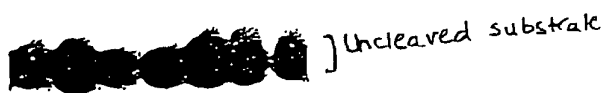


FIGURE 18

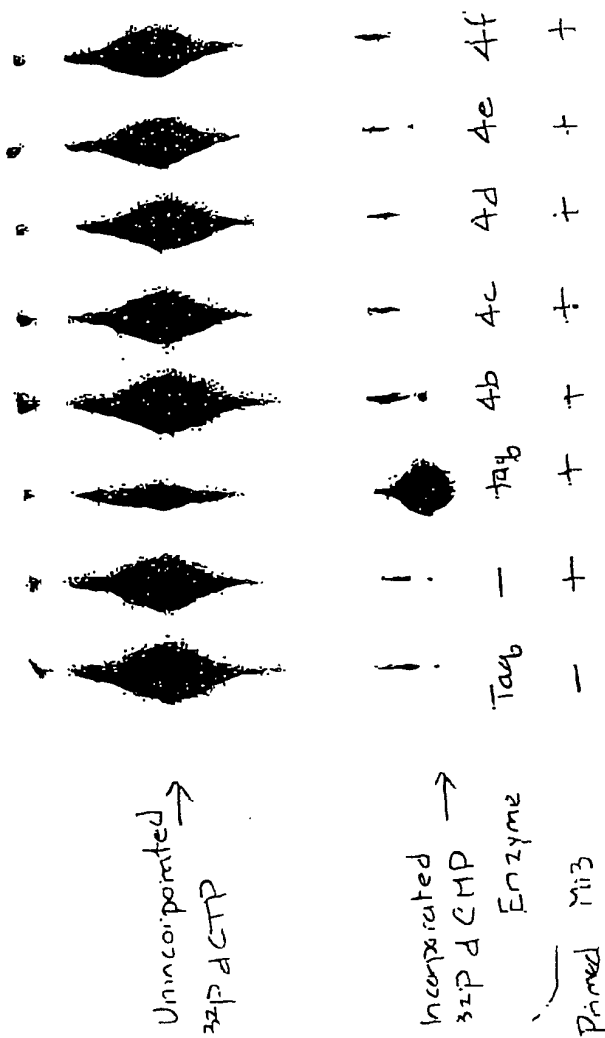
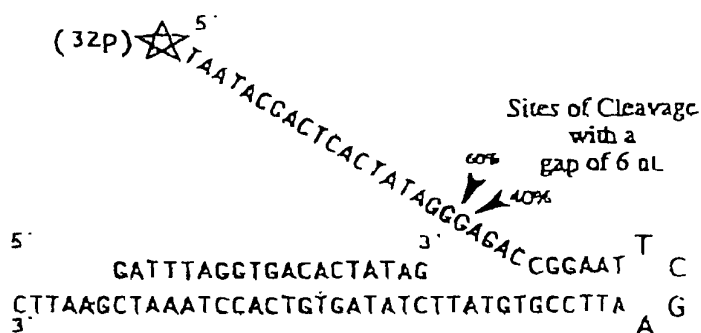


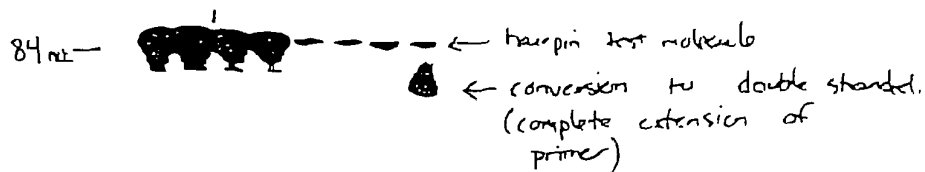
FIGURE 19

A

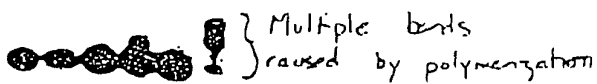


B

4d				4b		Unmodified	
No				(2 pr. mutation)		DNAT Tag	
Rel. Activity				small activity			
1	2	3	4	5	6	7	8
C1a				T1a		T2a	
+				+		+	



desired product  
21 nt.



some aberrant cleavage with 4b because of residual polymerase activity.

Hand-drawn diagram illustrating the A-T hairpin model for the T4 phage tail. The diagram shows two hairpin structures: an A-Hairpin and a T-Hairpin.

**A-Hairpin:**

- Top strand (5' to 3'): `CGGACGAACTAAGCGACACACCGACACAG`
- Bottom strand (3' to 5'): `GTACG C CATGG A T`
- Label: "Tau"

**T-Hairpin:**

- Top strand (5' to 3'): `GTTTCTCCGTCTCTCTCTCTT`
- Bottom strand (3' to 5'): `CTACTGTTCCCTCTCTCTCTGTC`
- Label: "Alpha"

Arrows indicate the predicted cleavage sites at the junctions of the hairpins. A dashed line connects the two hairpins, labeled "Predicted cleavage sites".

C

5' ACACAGT A

GTACC C

CATGC A

T

"Tau" →

5' CAAACACgACACAGCAGAgAgAACCCACAA' T

Cleaved A-Hairpin

5' TCTCTTT A

GTACC T

CATGC G

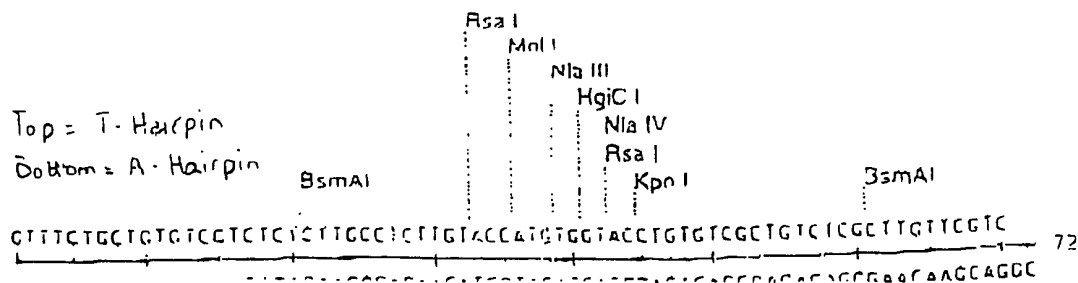
T

"Alpha" →

5' -CTGCTGTTCCTCTCTGTCCCTGTGTC- T

Cleaved T-Hairpin

D



Ban II  
 Sst I  
 Asp 718  
 Ava I  
 Kpn I  
 Xma I  
 Sma I  
 Bam HI XI  
 EcoR I  
 T7  
 -47 Forward  
 Pst I  
 Sal I  
 Acc I  
 Hinc II  
 BspMI  
 Sph I  
 Hind III  
 PUot 30-0  
 -48 Reverse  
 206

FIGURE 22A

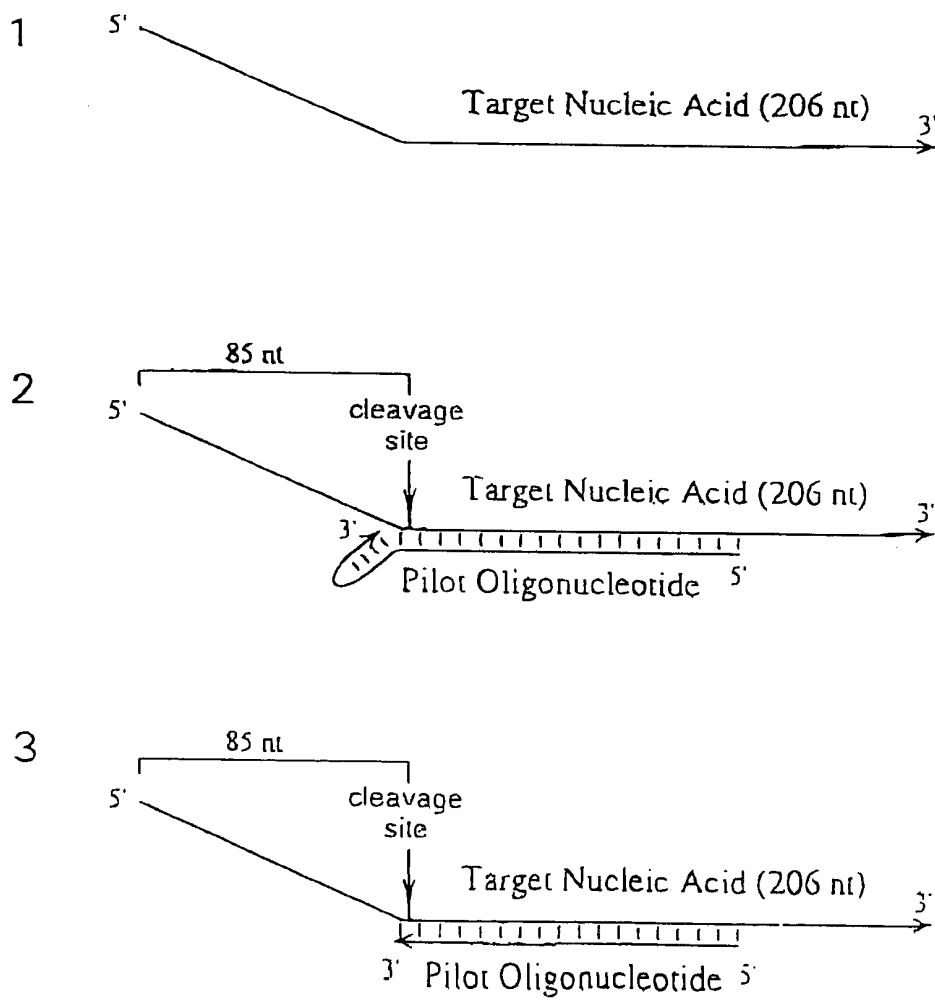






FIGURE 23

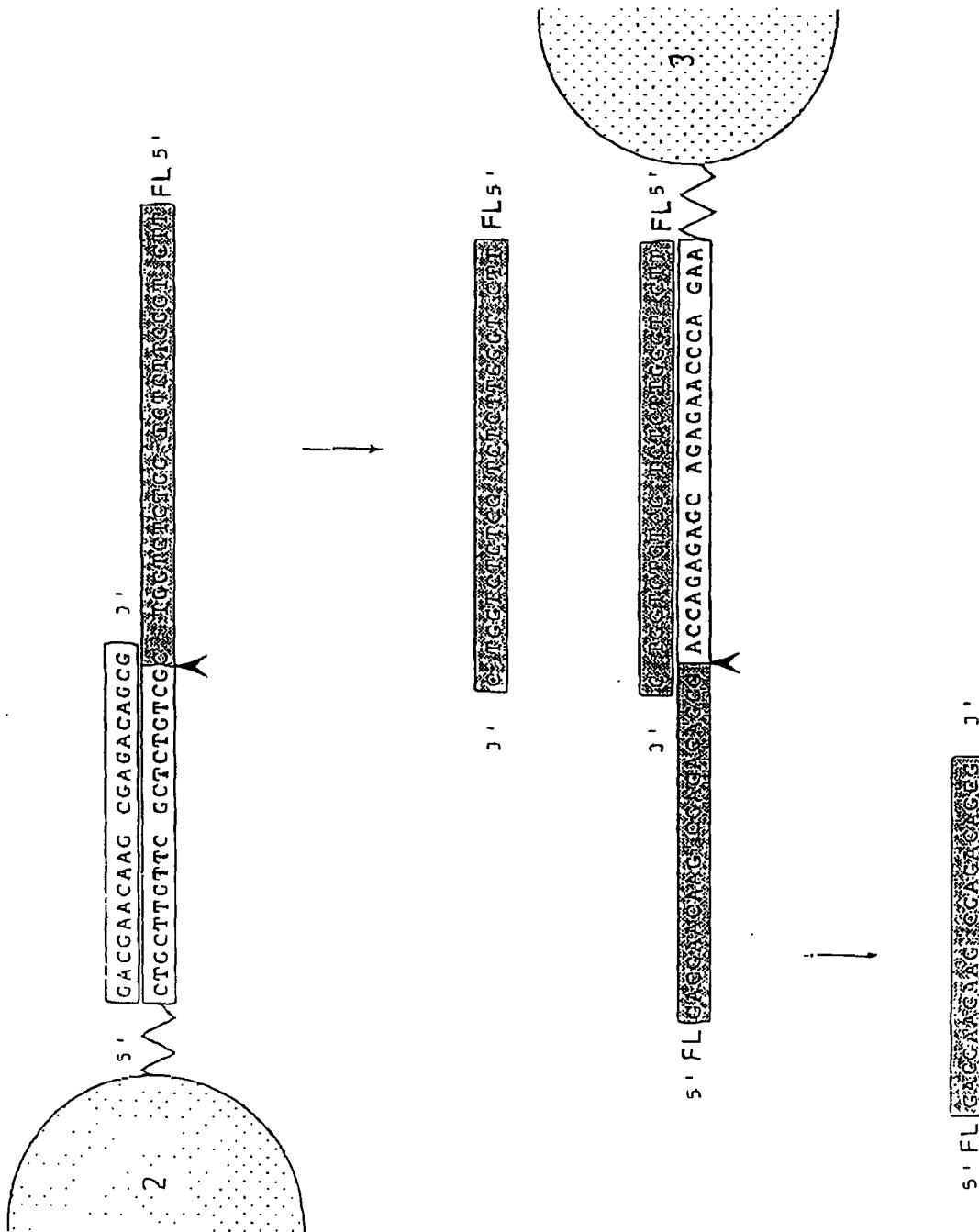




FIGURE 25

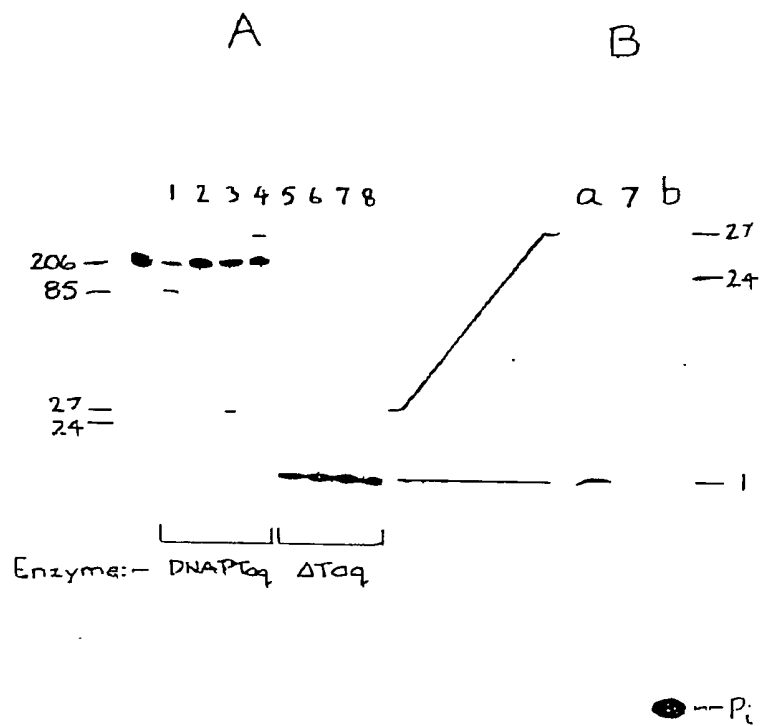
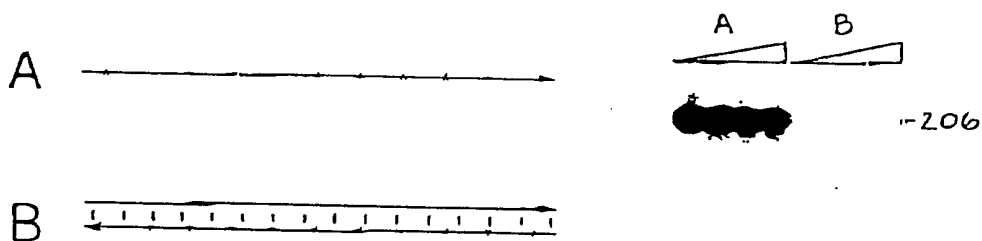


FIGURE 26



$\approx 32\rho$

FIGURE 27

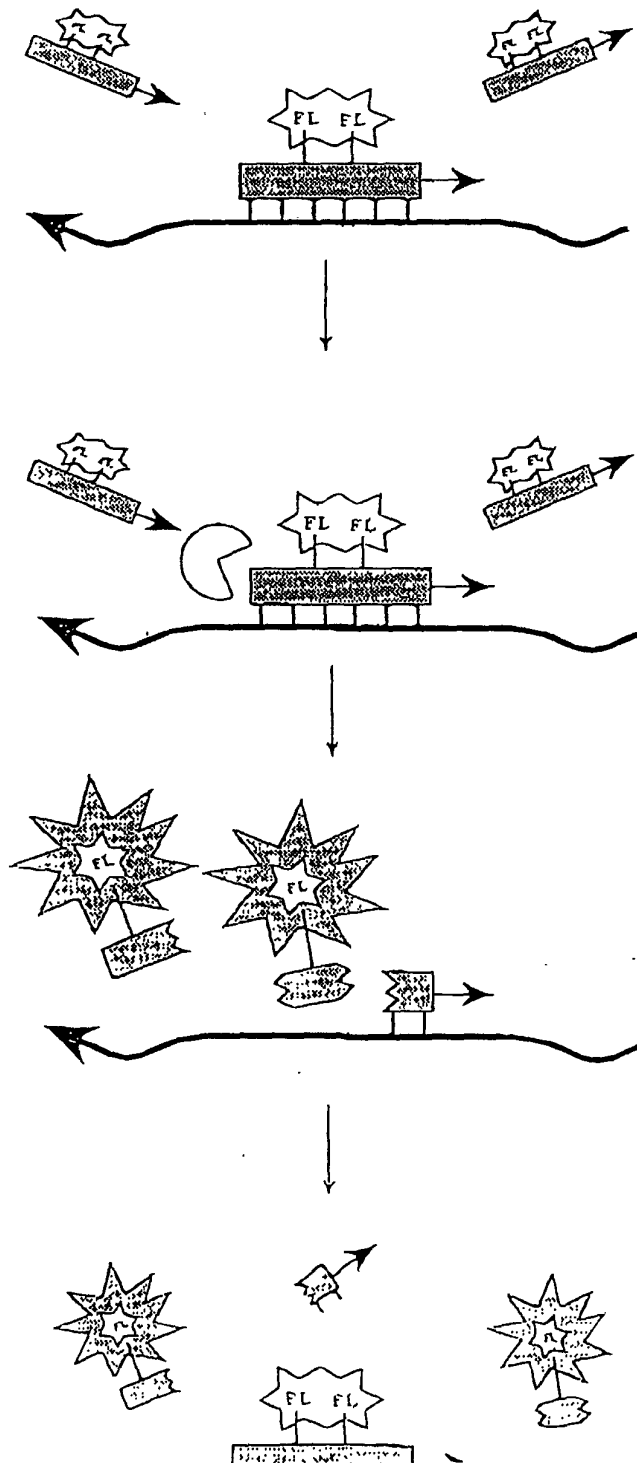
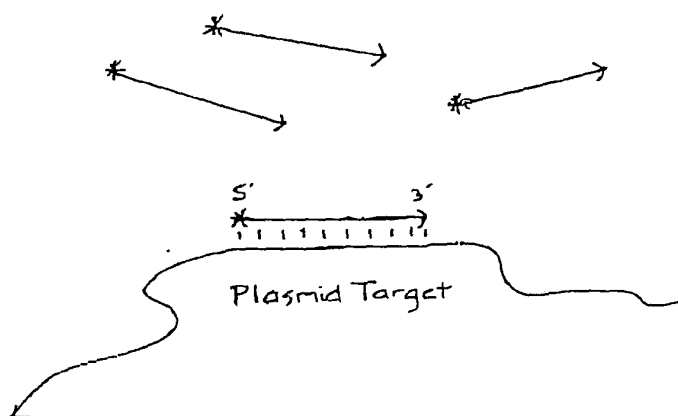
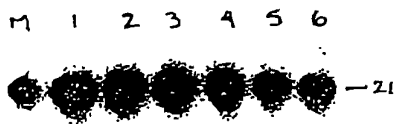


FIGURE 28A



\* =  $^{32}\text{P}$  5' terminal phosphate

FIGURE 28B



-1



FIGURE 29

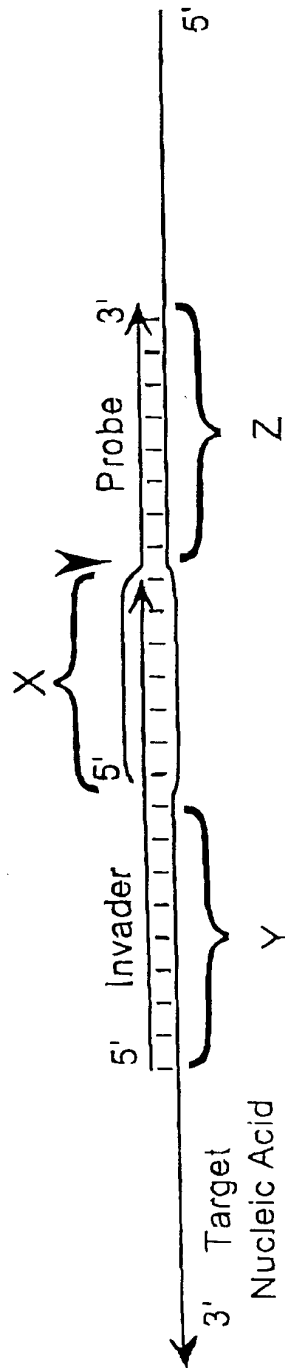


FIGURE 30

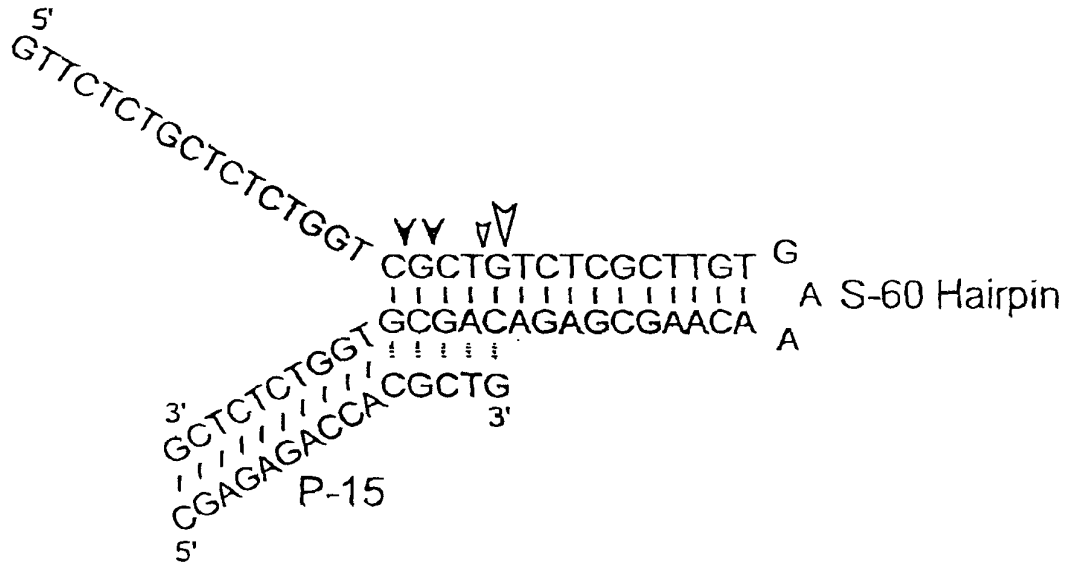


FIGURE 31

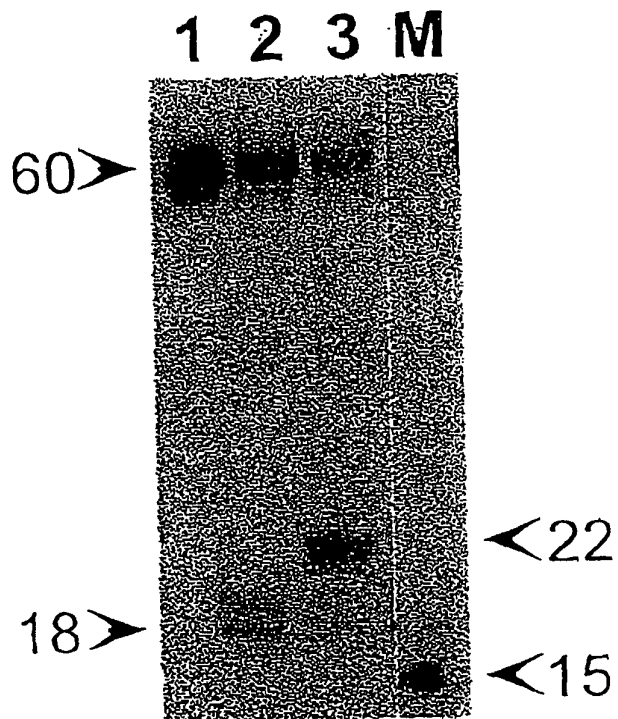
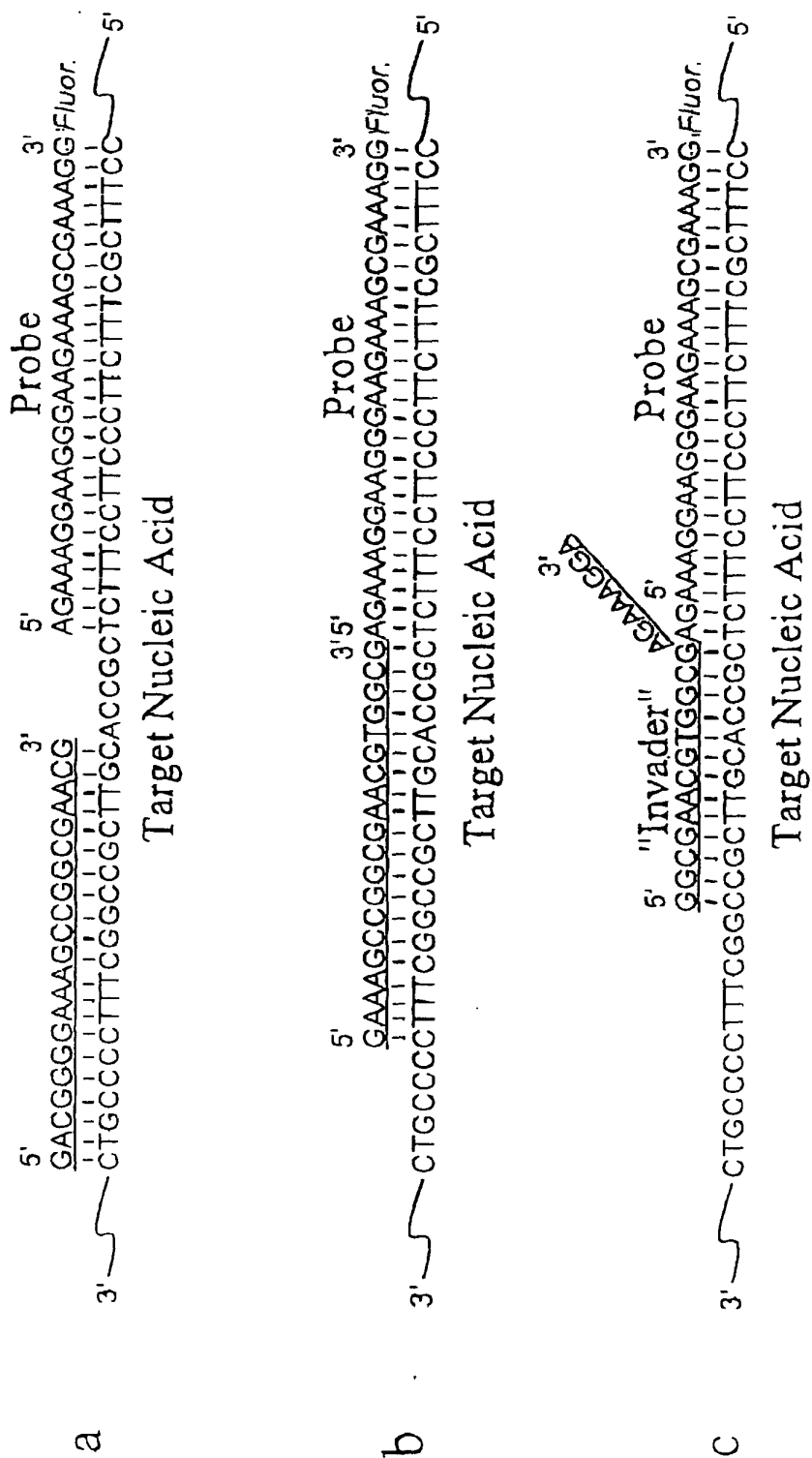
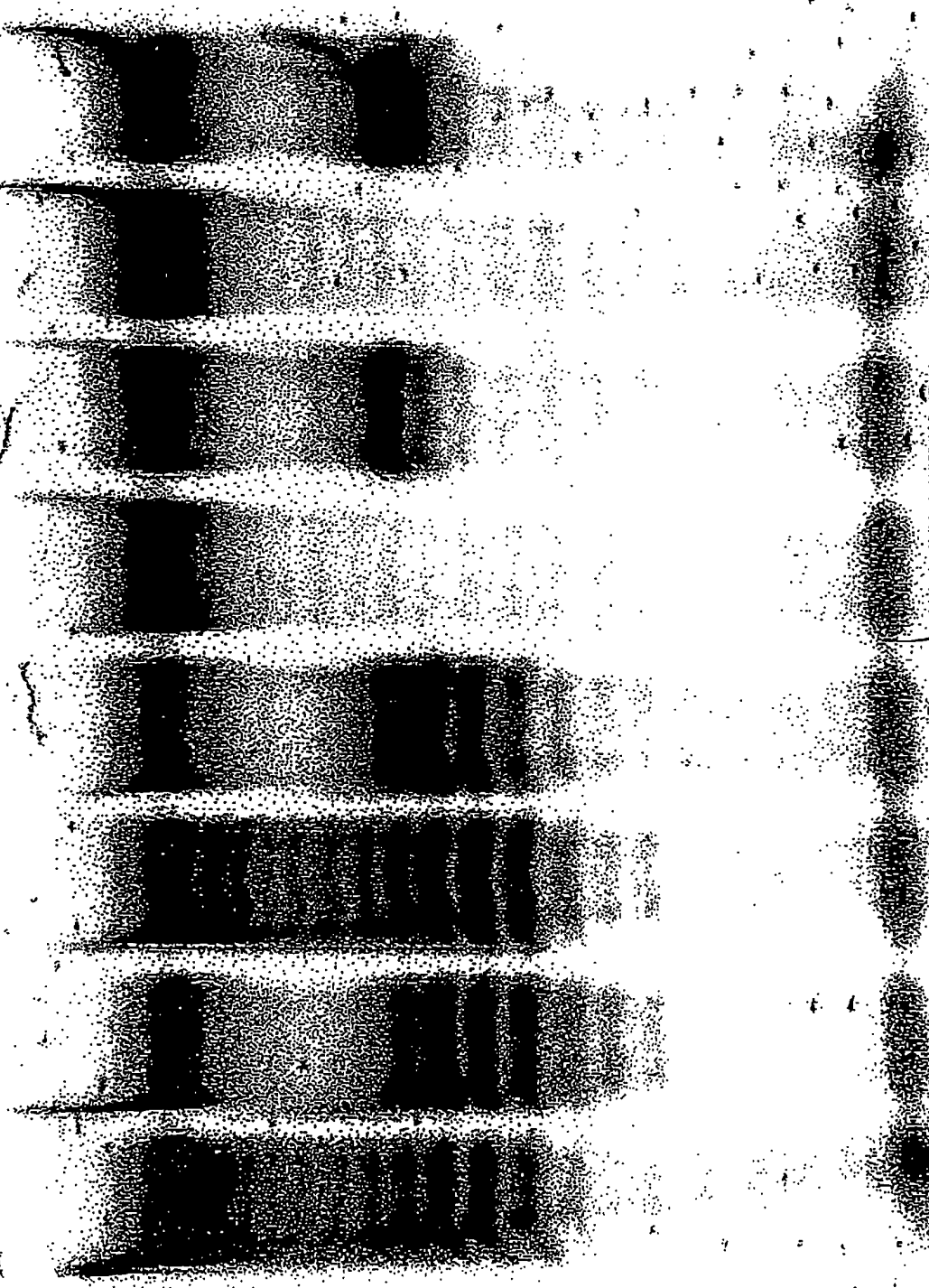


FIGURE 32



1 2 3 4 5 6 7 8

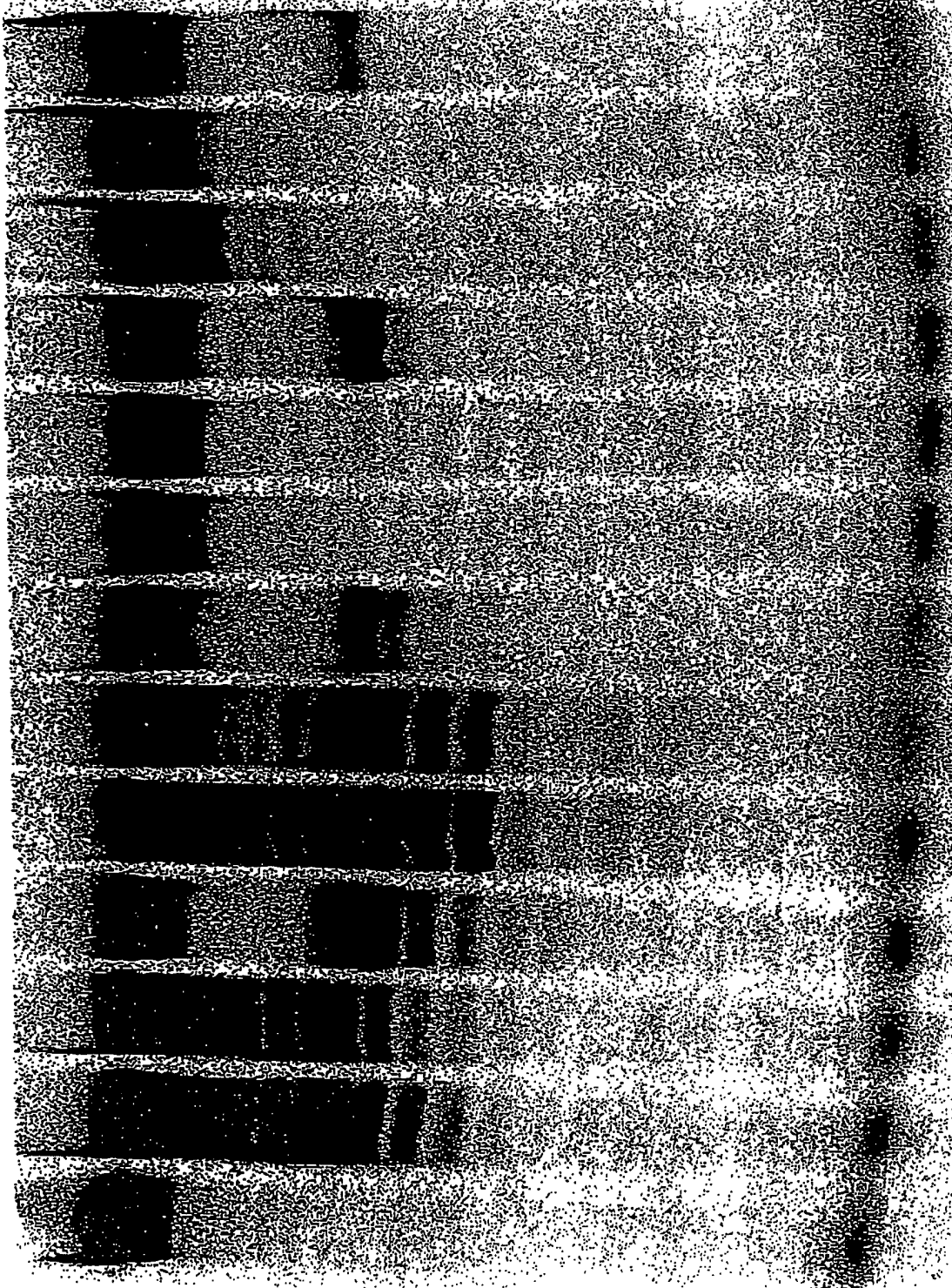


6

45

FIGURE 34

M 1 2 3 4 5 6 7 8 9 10 11 12



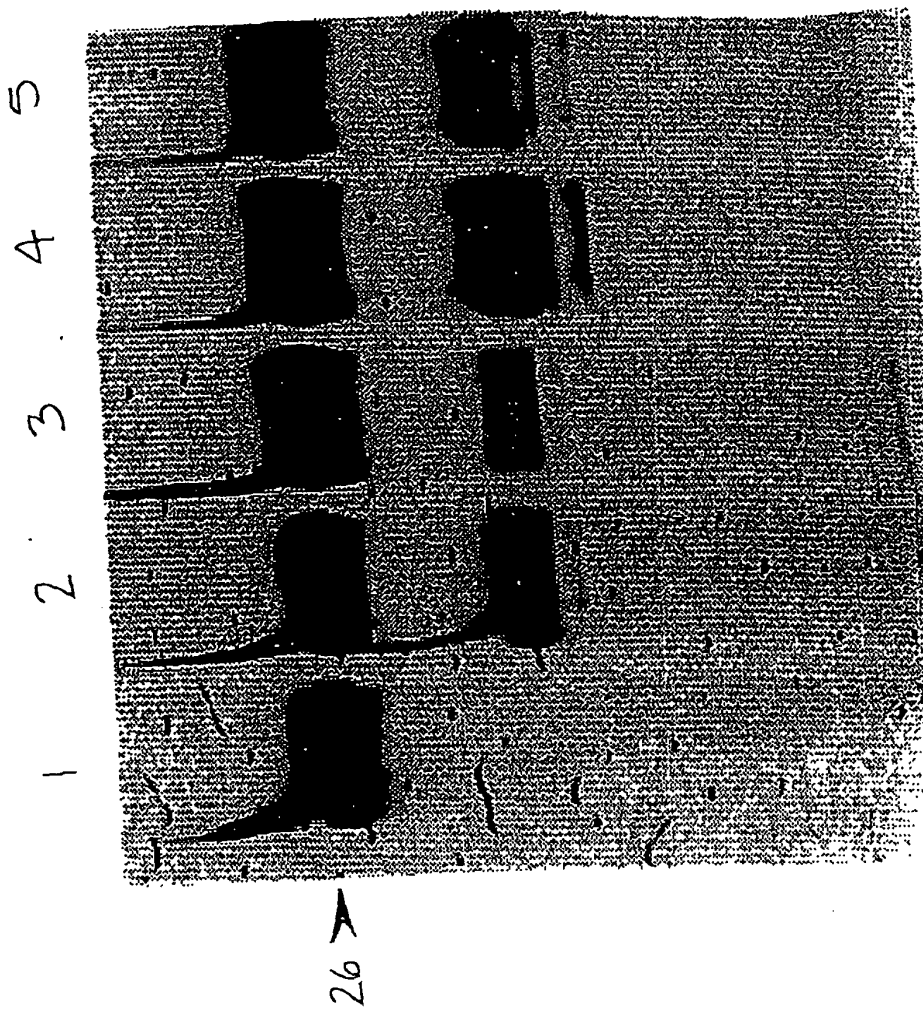
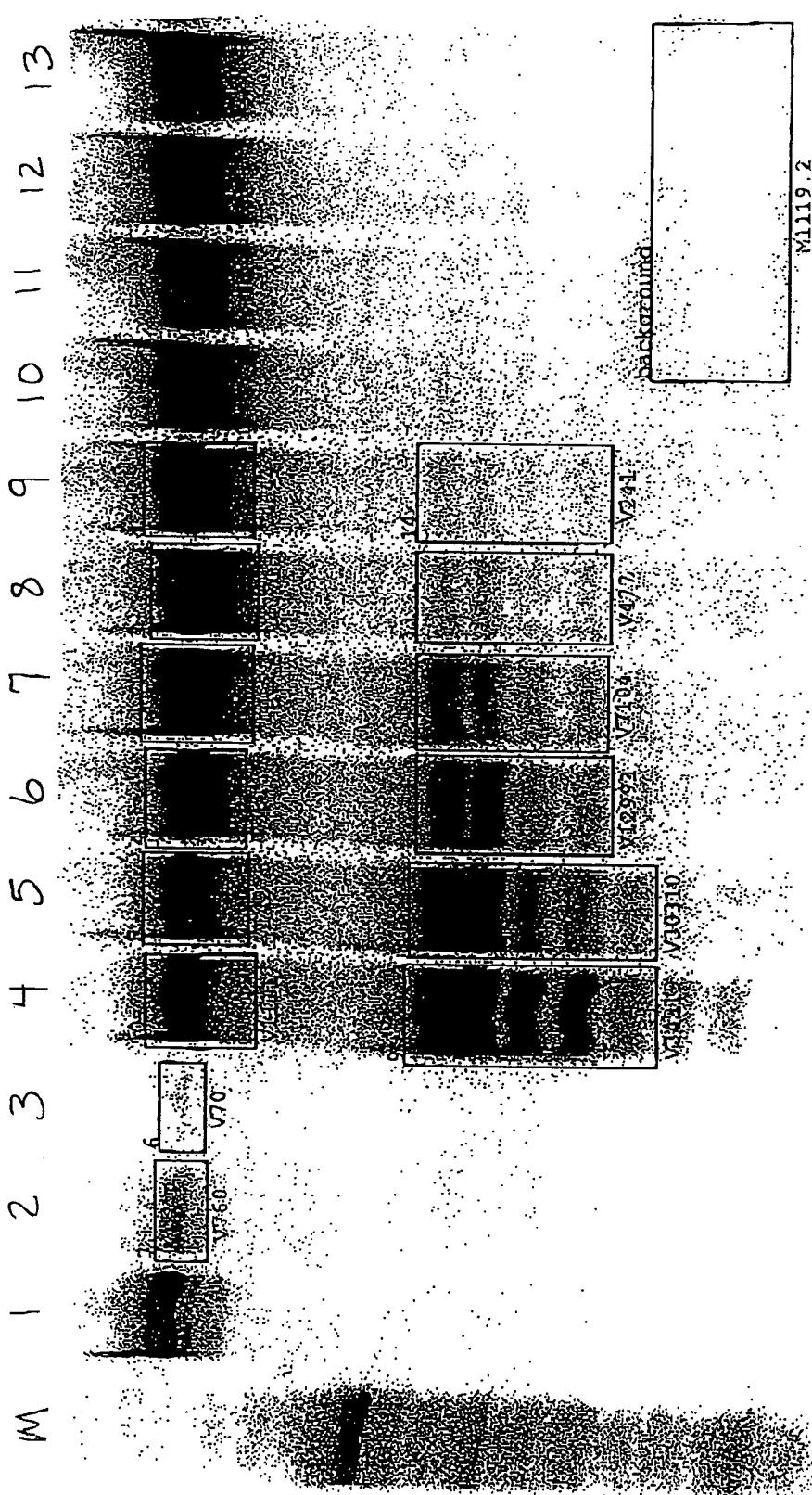
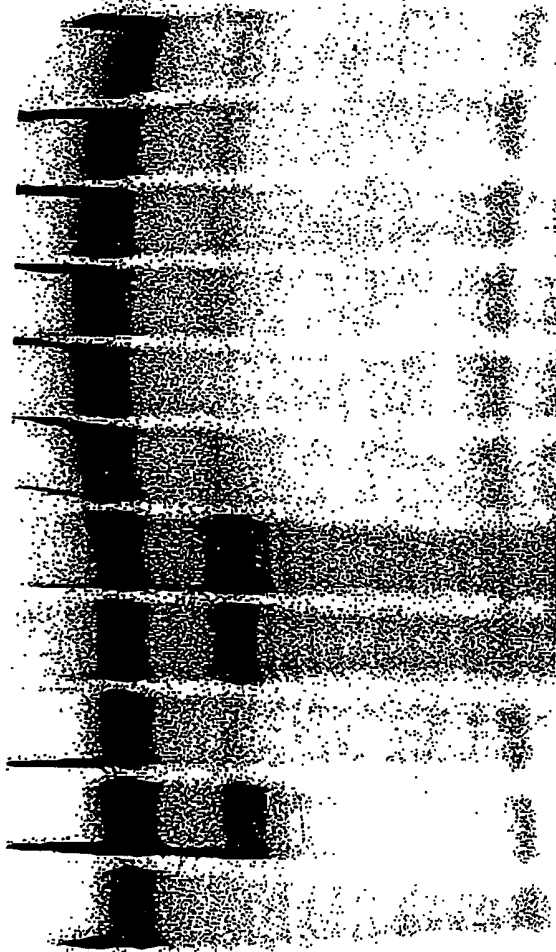


FIGURE 36





1 2 3 4 5 6 7 8 9 10 11



A A

FIGURE 38

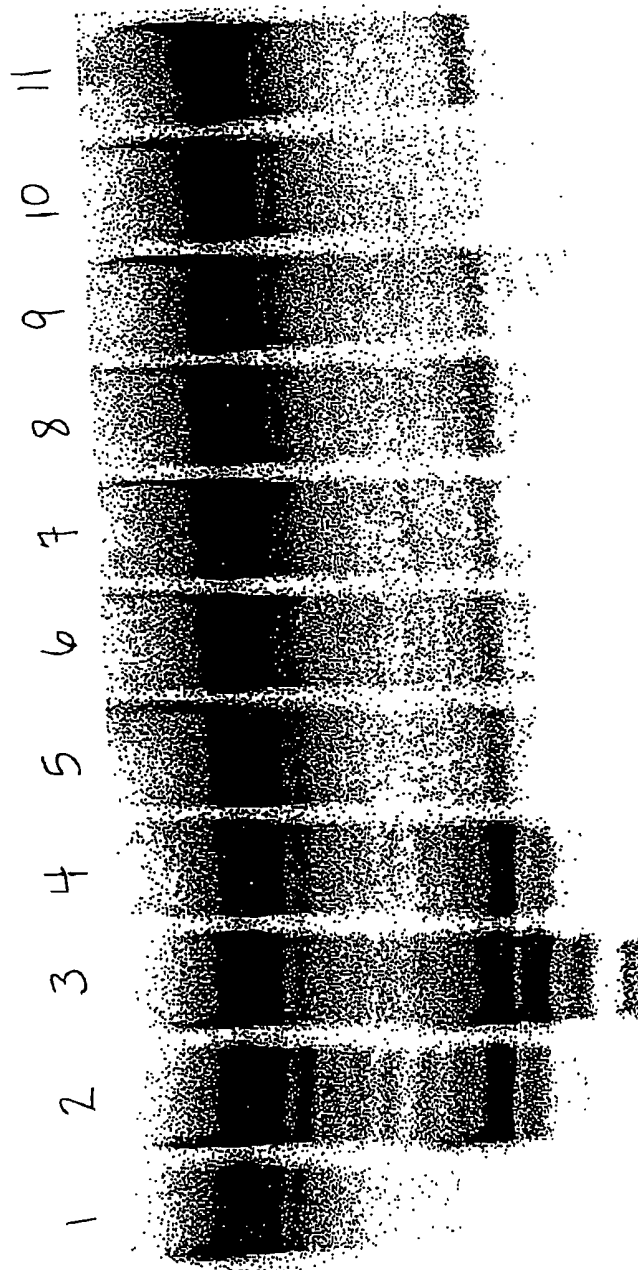


FIGURE 39

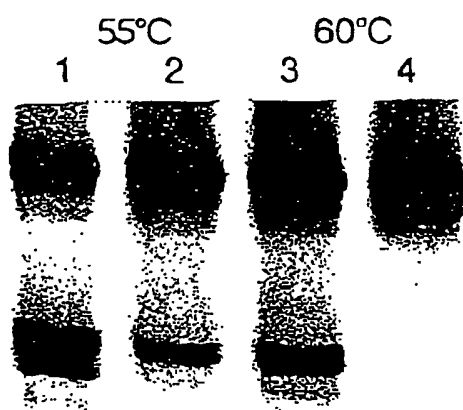




FIGURE 41

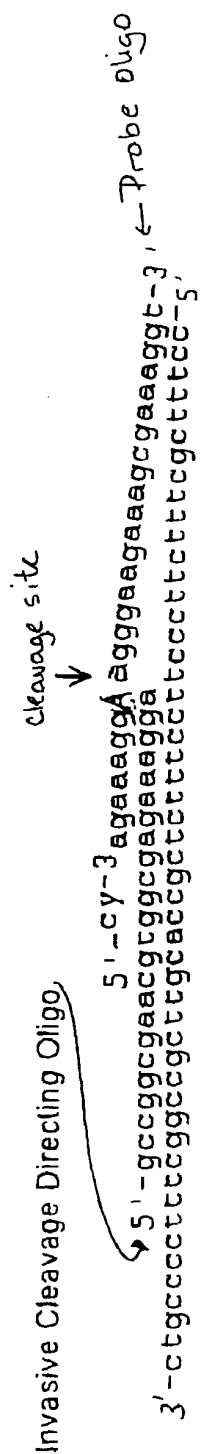


FIGURE 42

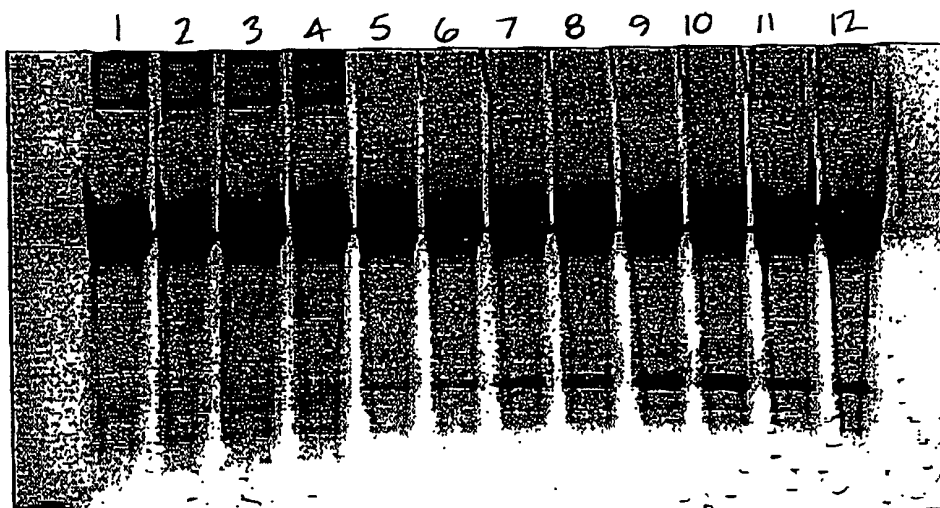


FIGURE 43

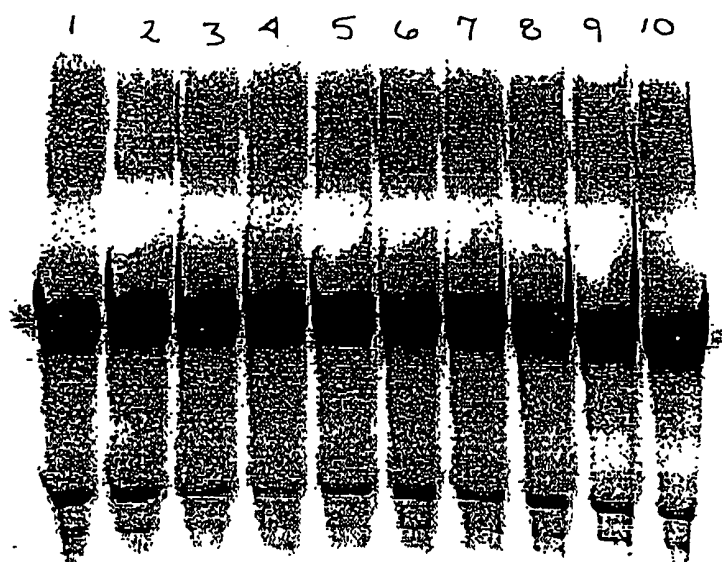


FIGURE 44

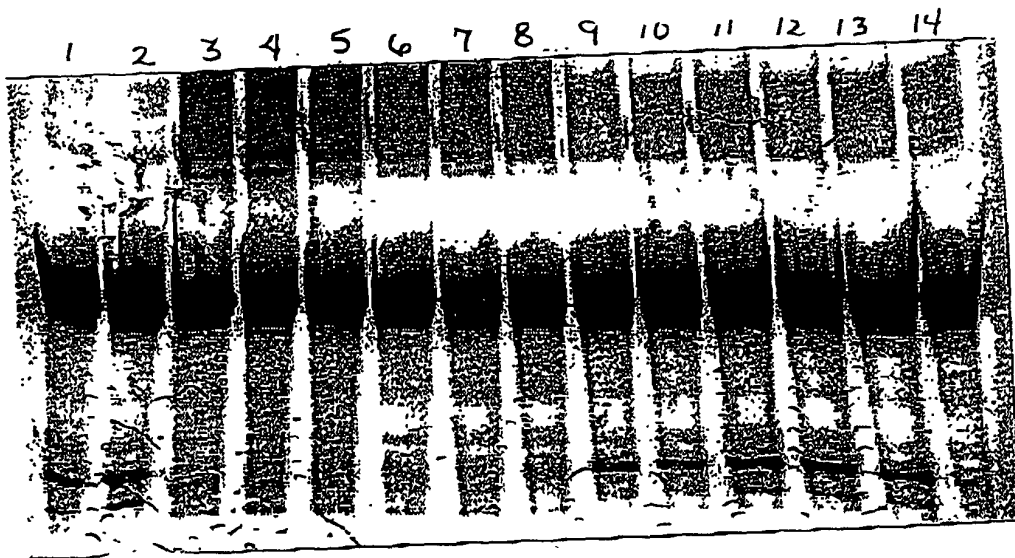




FIGURE 45

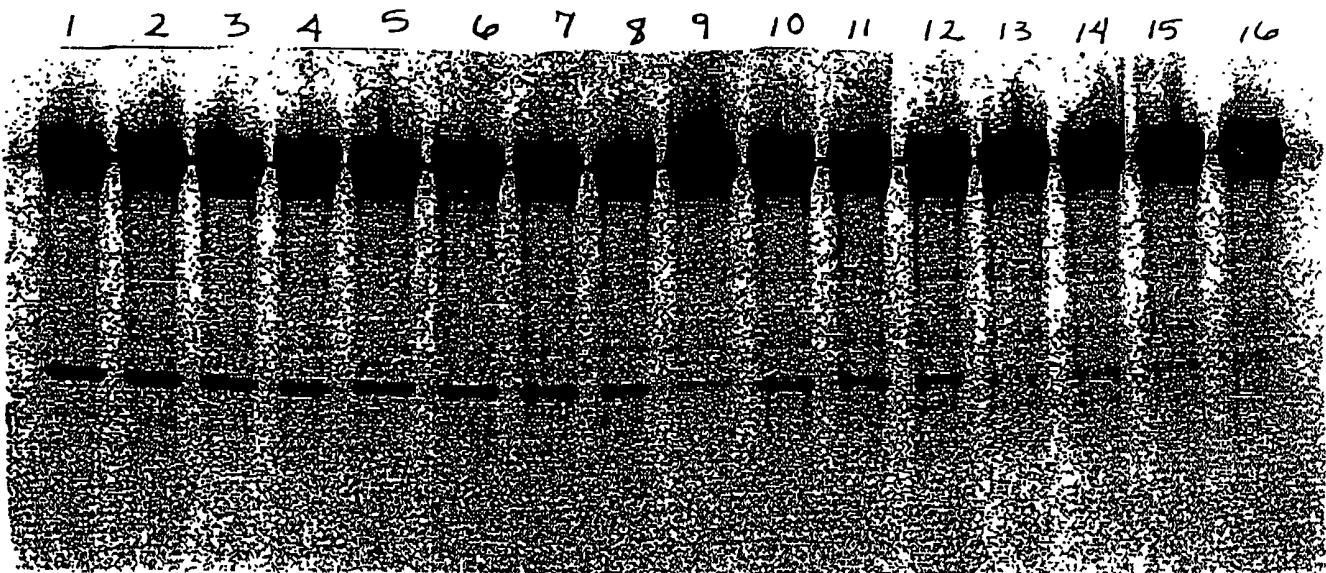


FIGURE 46

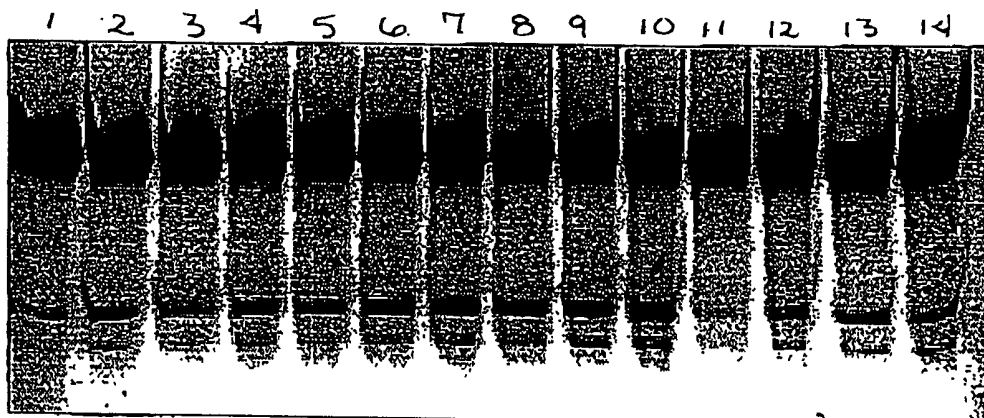




FIGURE 48

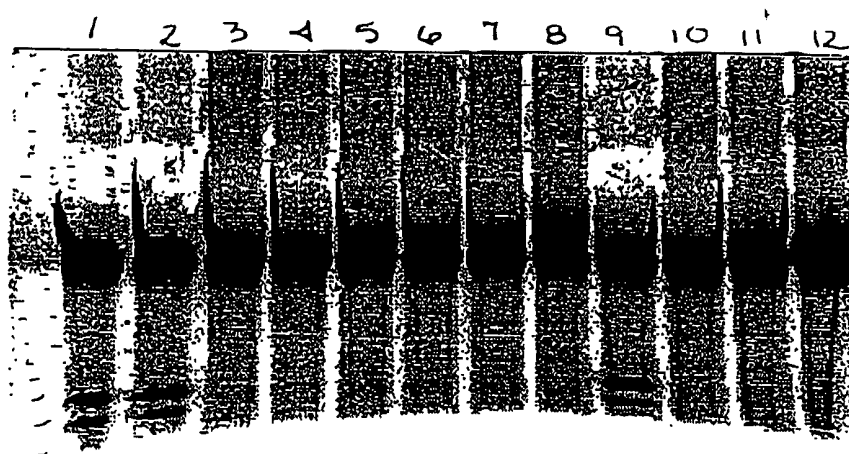


FIGURE 49

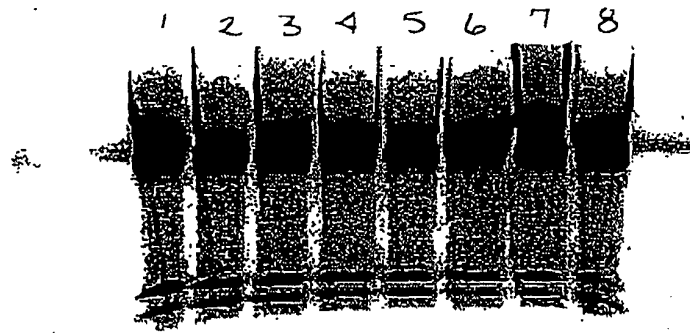


FIGURE 50

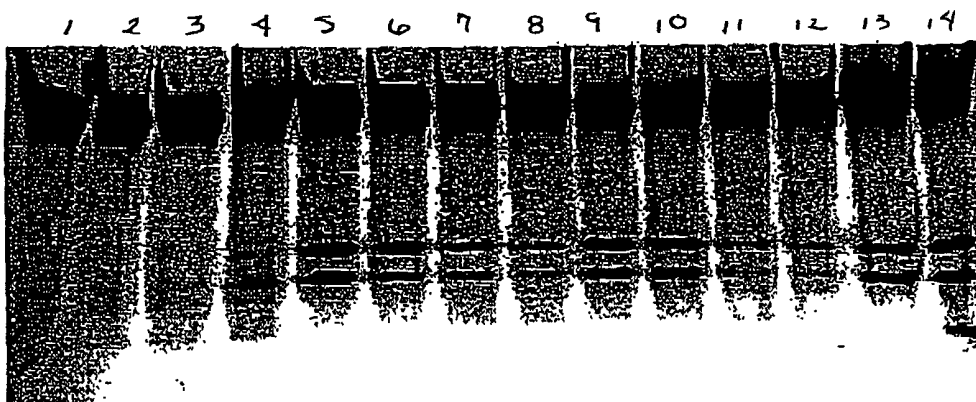


FIGURE 51

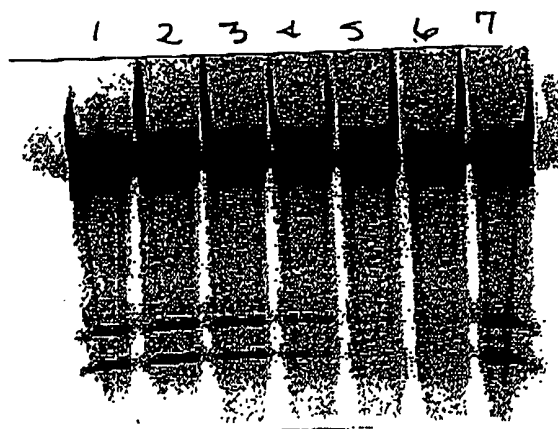






FIGURE 53

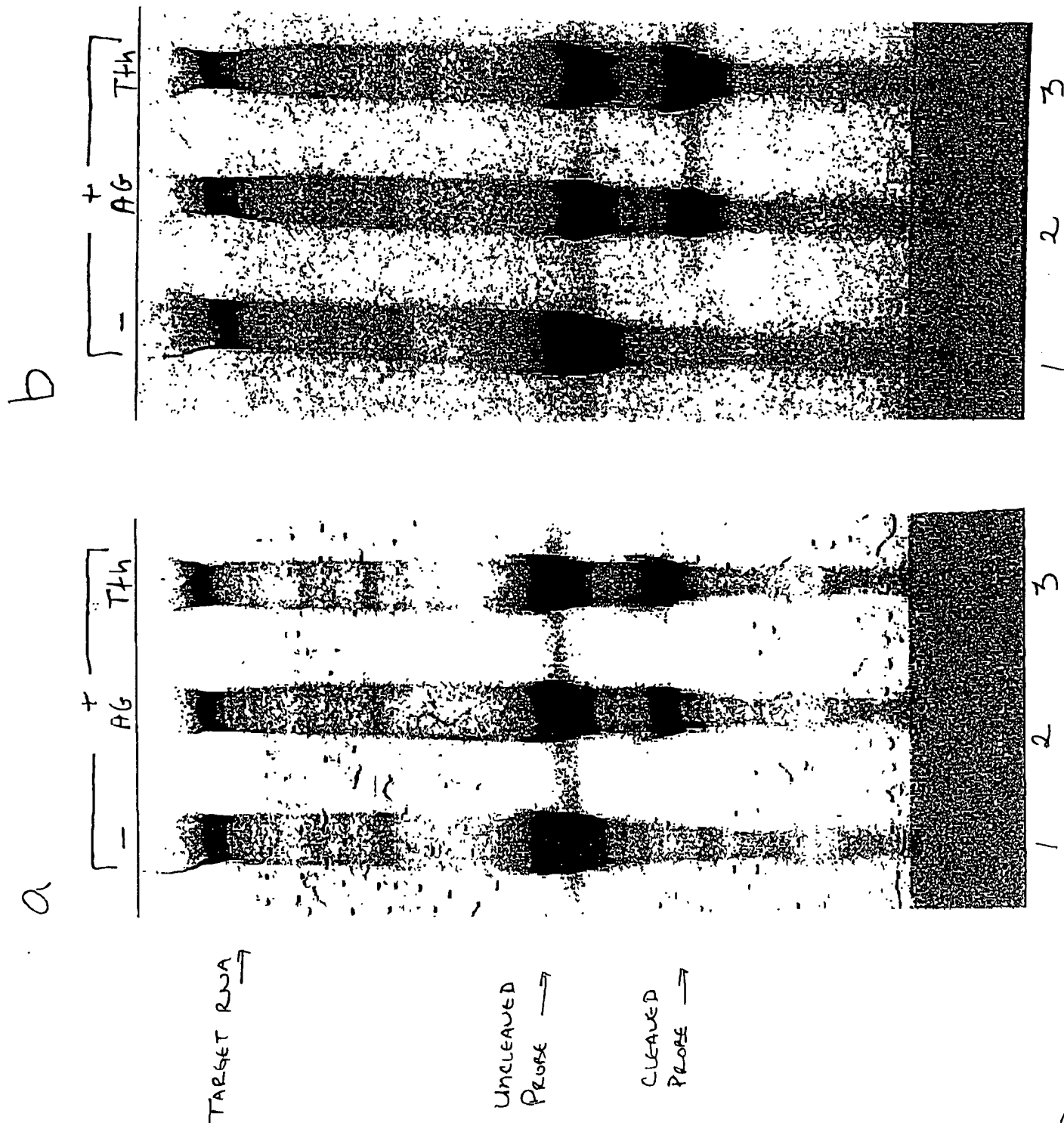




FIGURE 55



FIGURE 56

70 (C10 aminoT's)

74 (C6 amino T's)

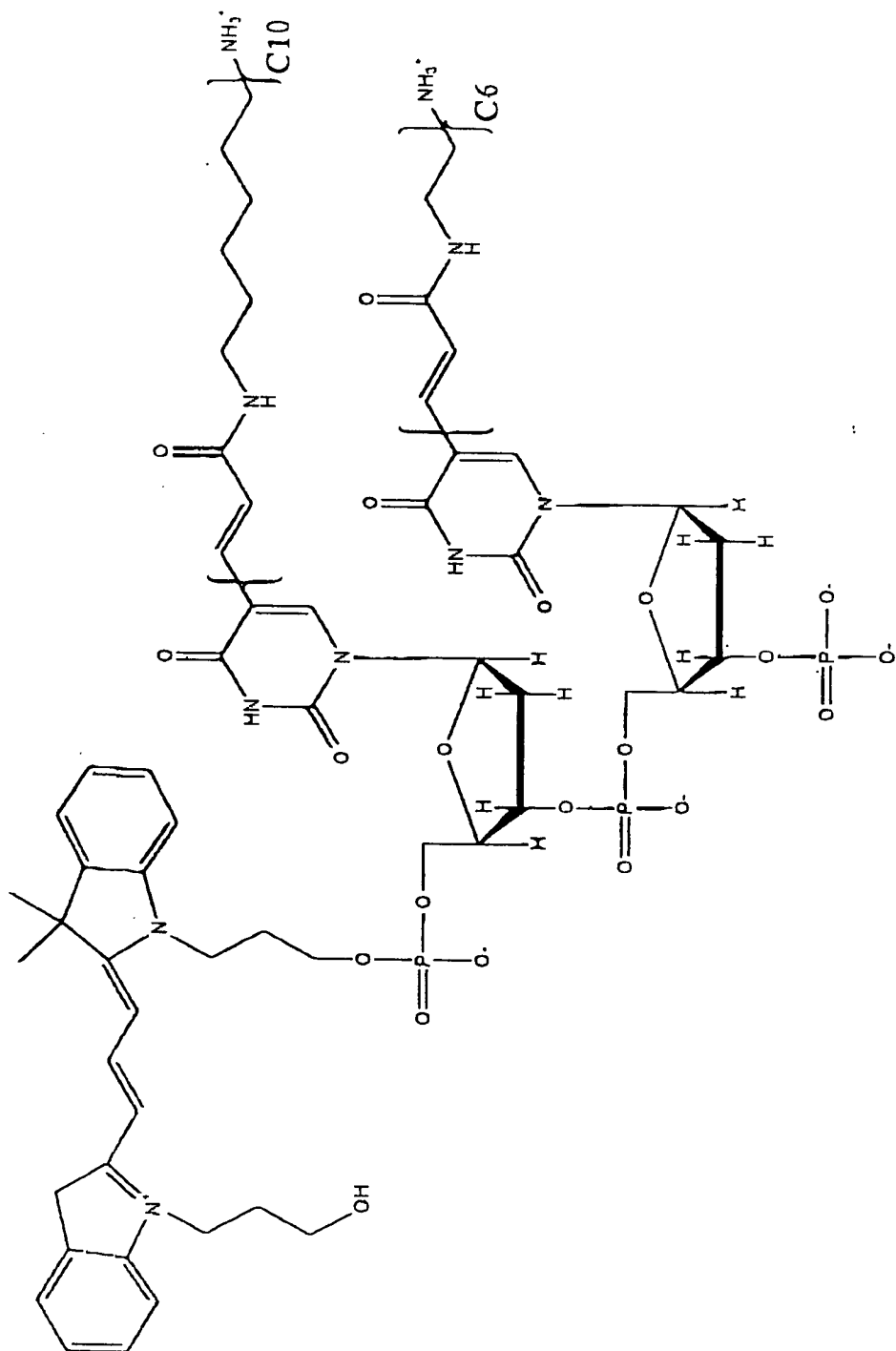


FIGURE 57

75

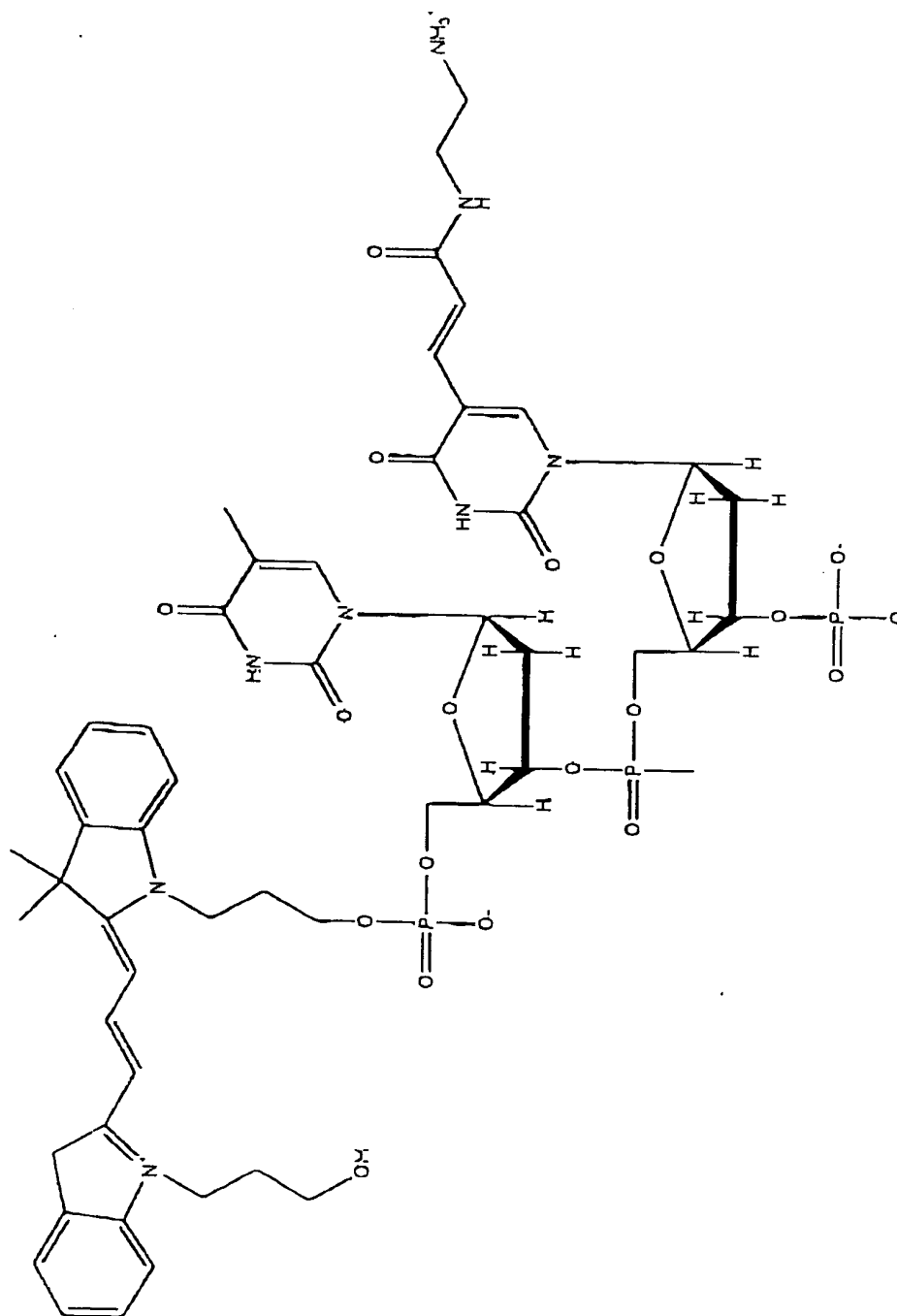
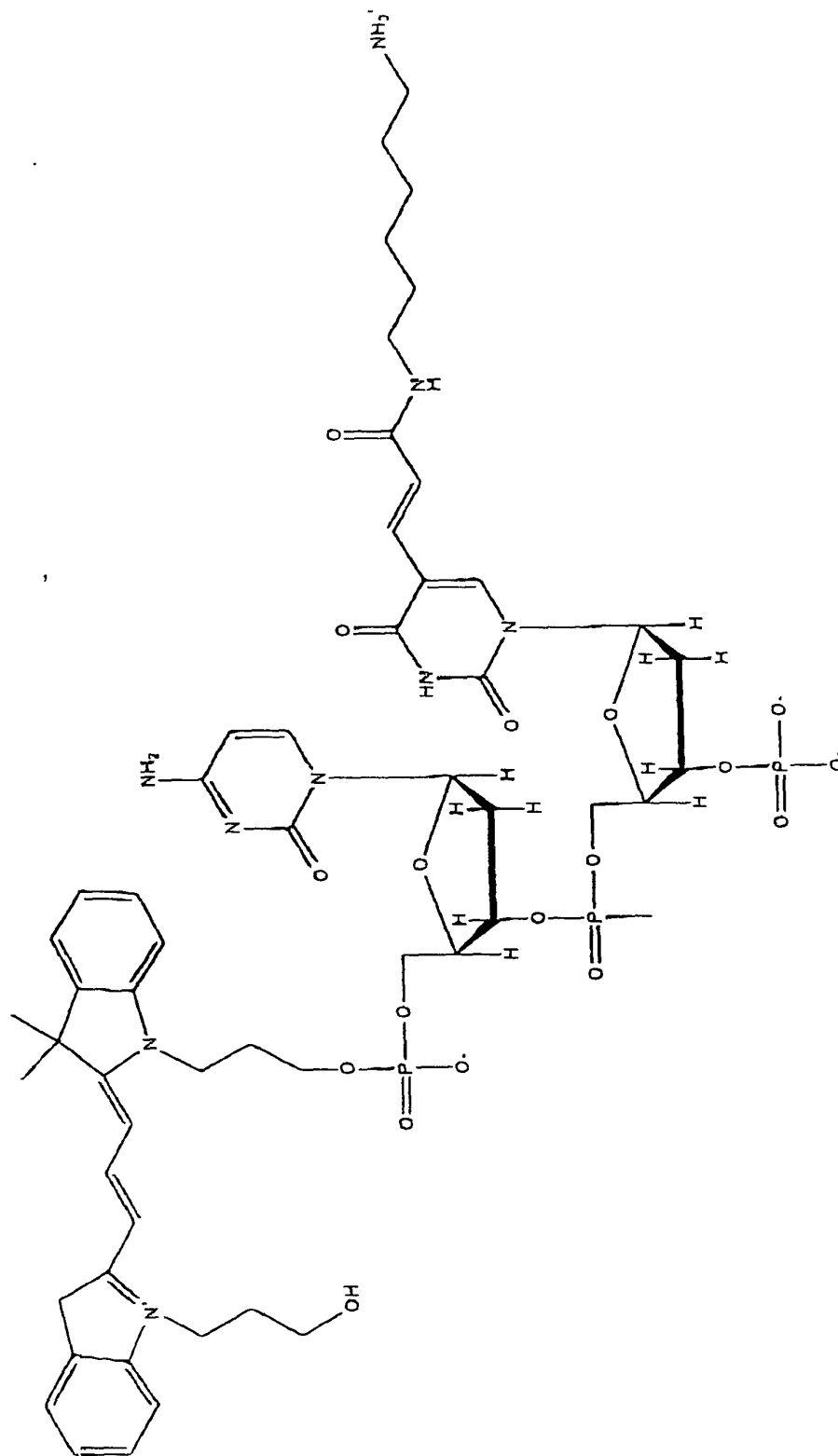


FIGURE 58

76



76

FIGURE 59

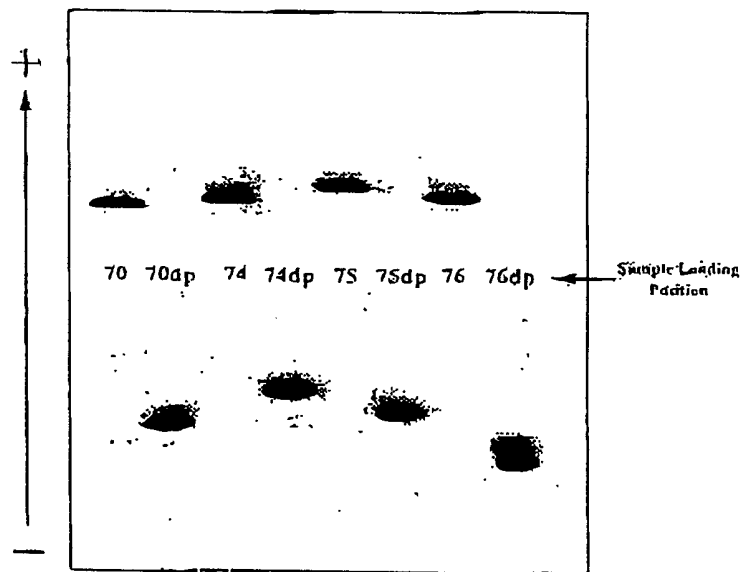
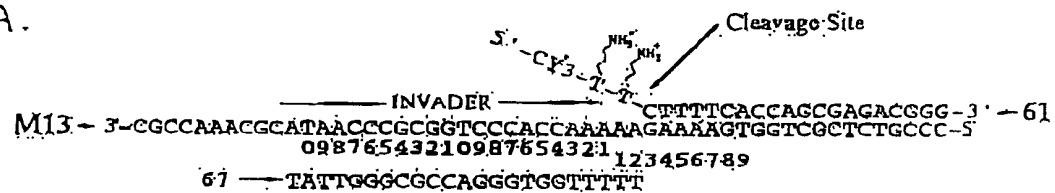


FIGURE 60

A.



B.

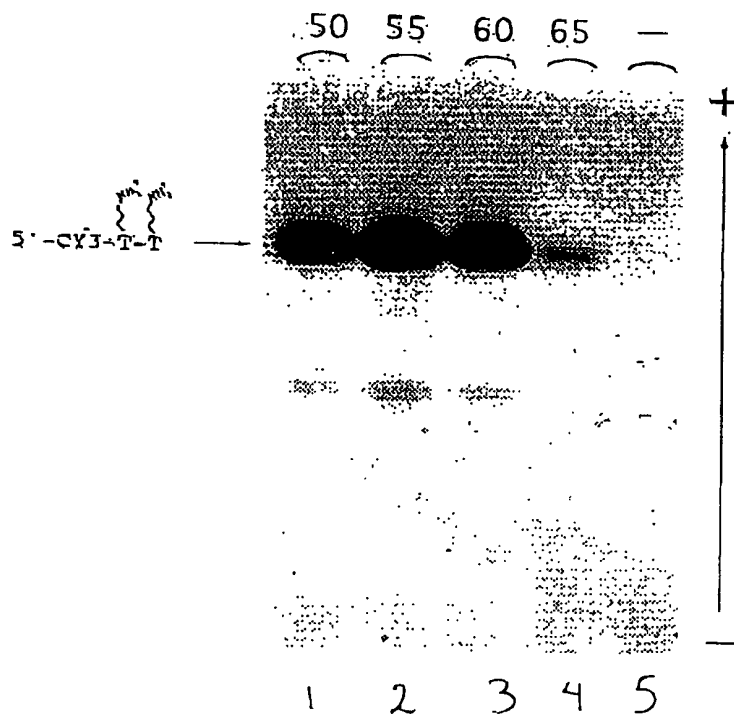




FIGURE 61

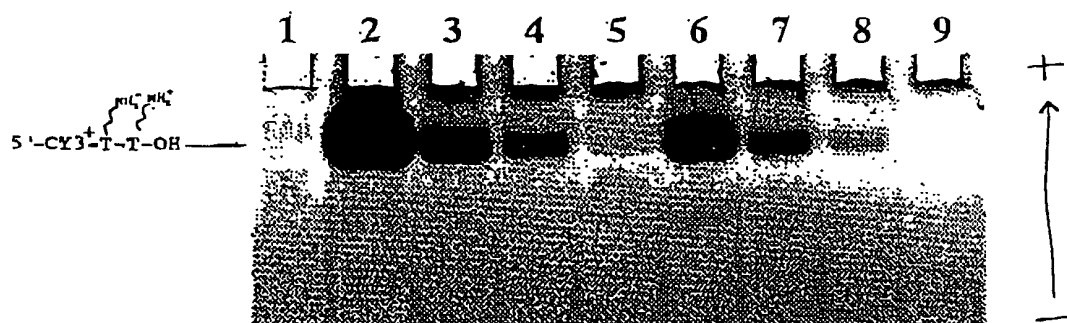


FIGURE 62

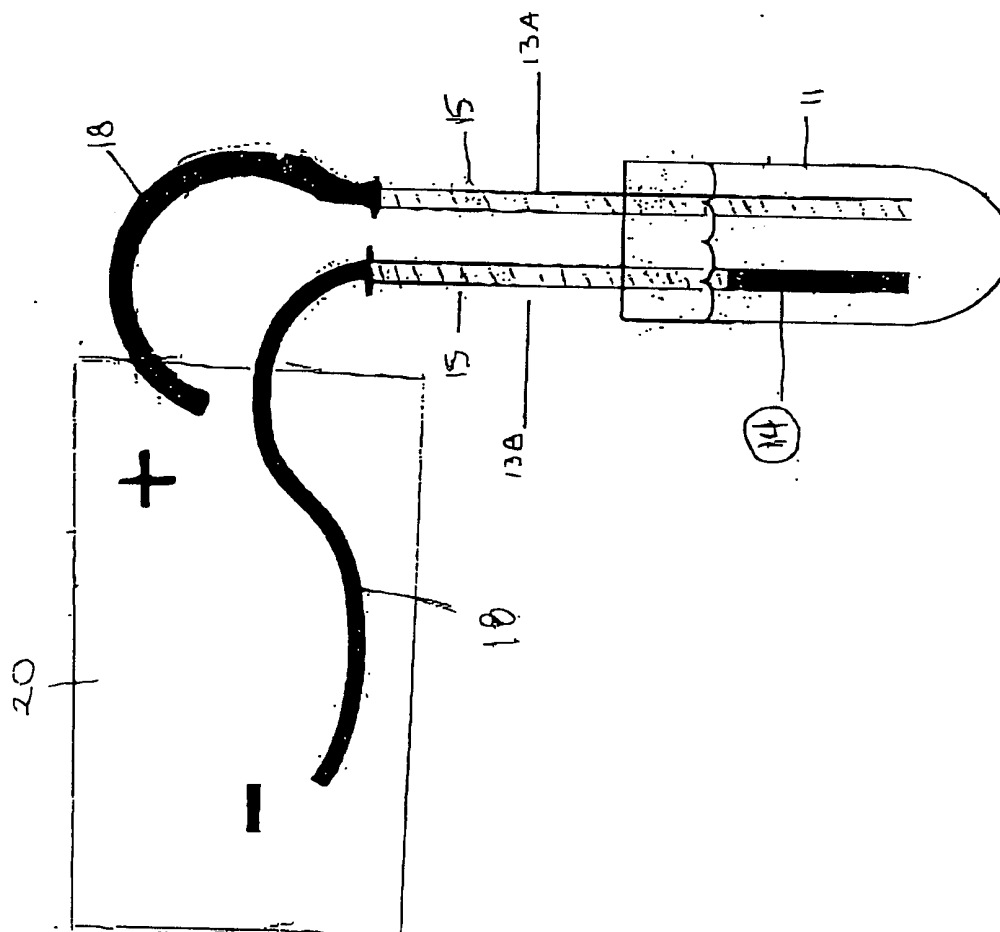


FIGURE 63

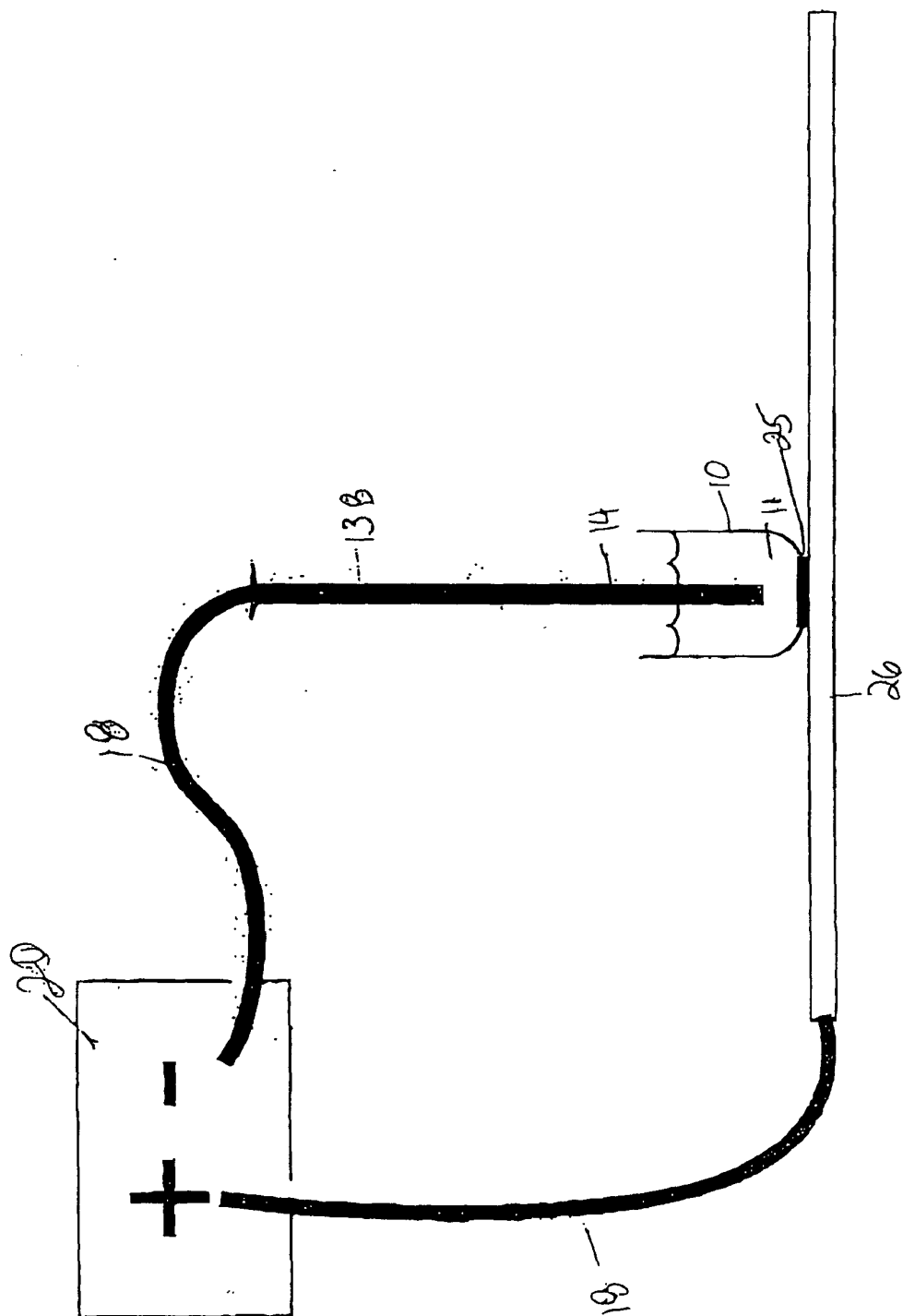


FIGURE 64



FIGURE 65



FIGURE 66

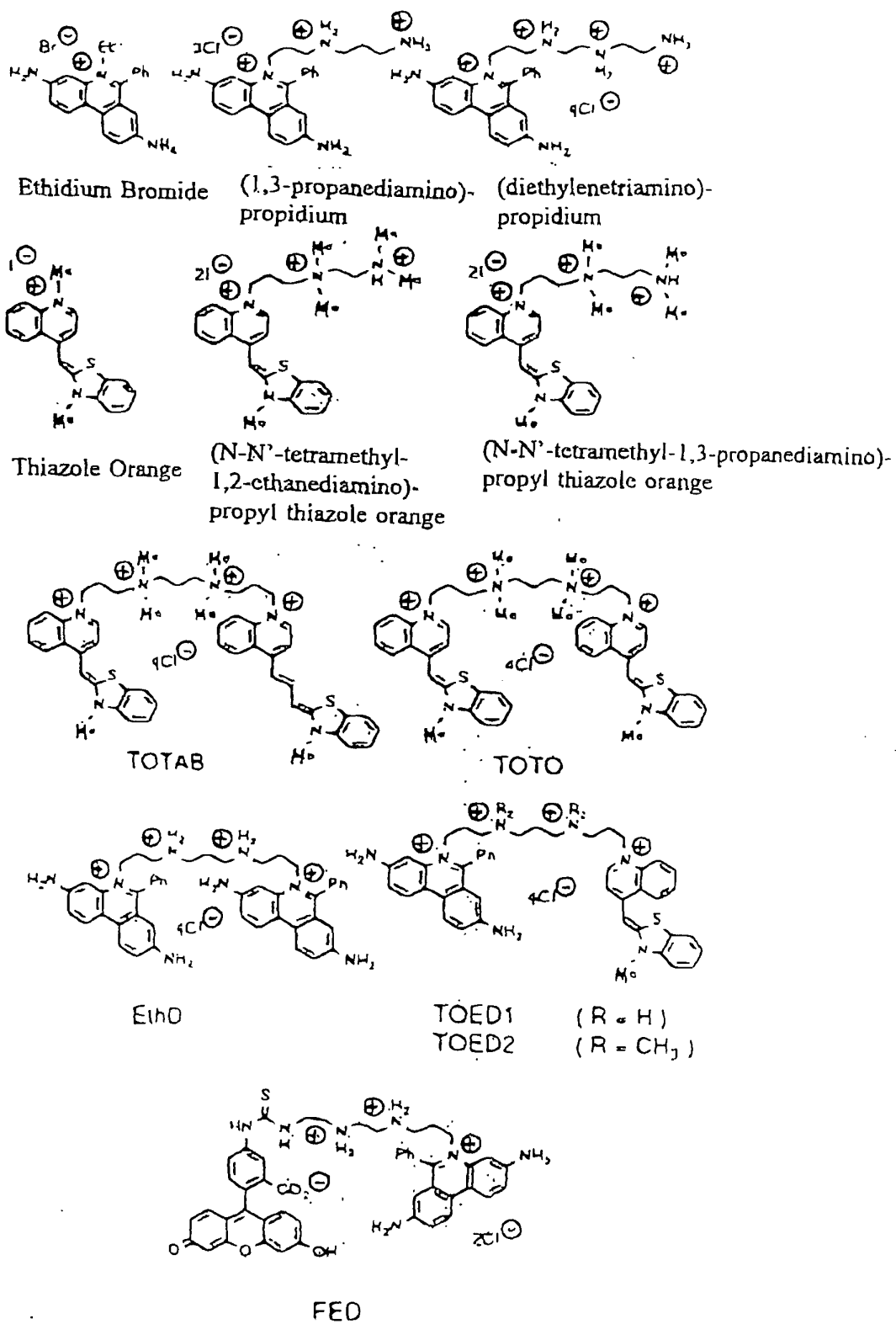


FIGURE 67

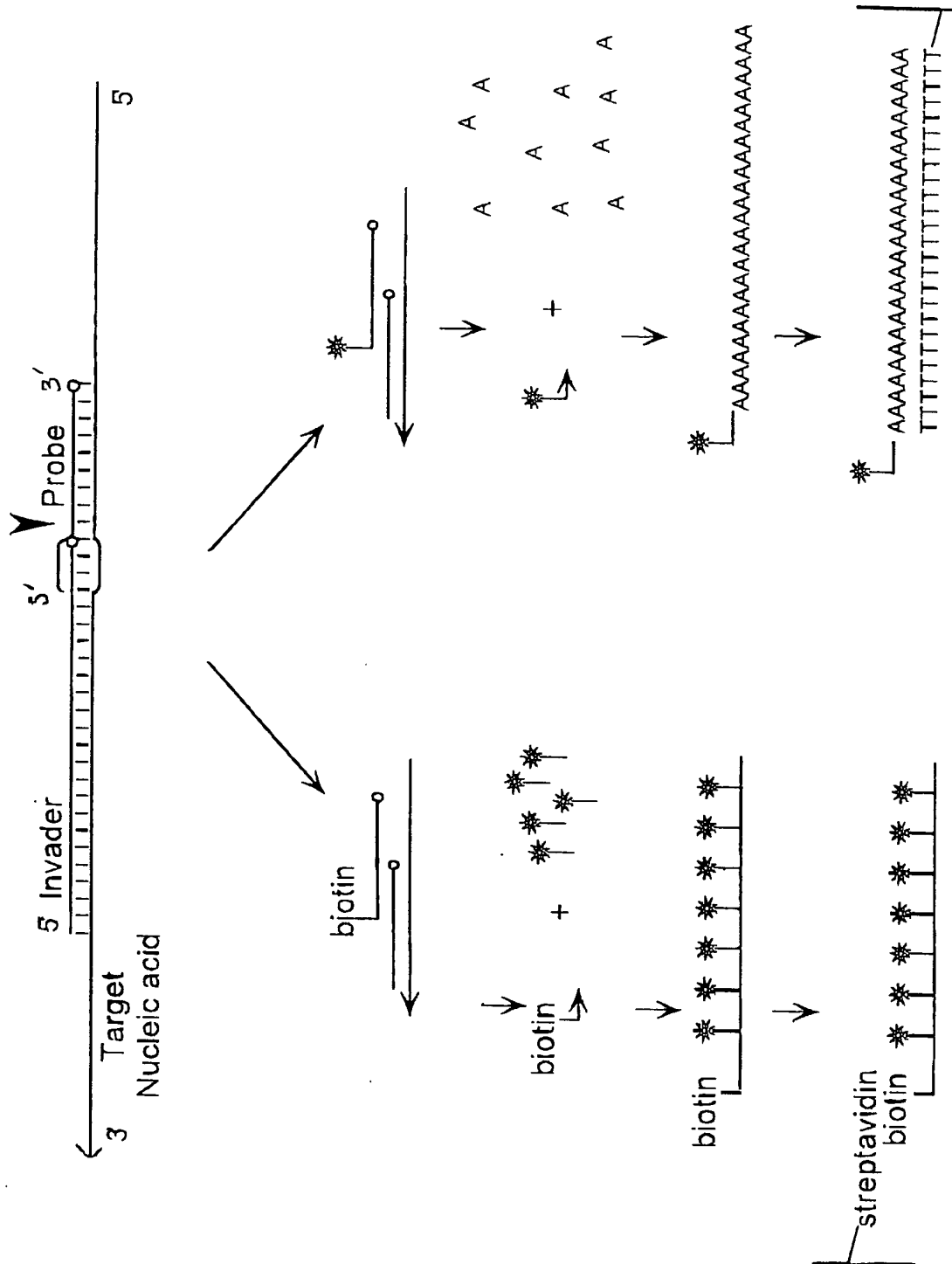
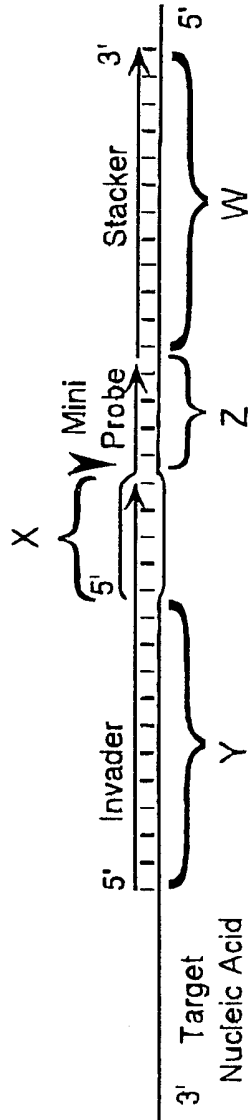
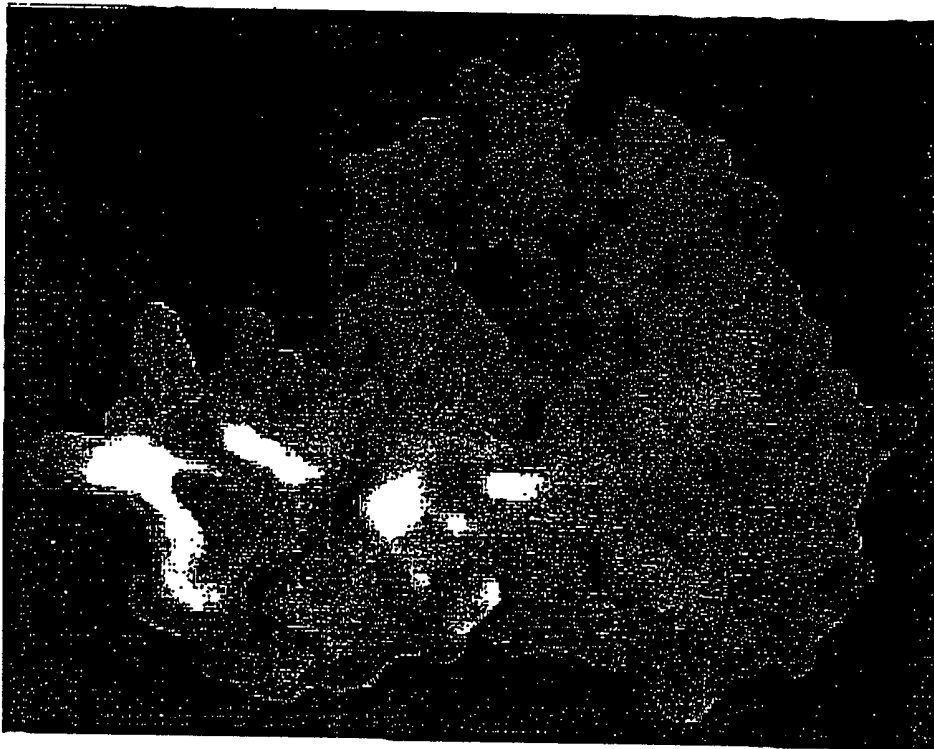


FIGURE 68





**FIGURE 69**



**FIGURE 70-A**

	10	20	30	40	50	60	70										
MGVO	----	FGDFJPK	--NI	ISFEDLKGKKVA	IDGMNAL	YQFLT	SIRLRDGSPLNRKGE	ITSAYNGVFY	MJAFEN1	.PRO							
MGVP	----	IGE1	IPR	--KE	ELENLYGKK	AIDALNA	IYQFLT	IROKDGTP	MDSKGR	ITSHLSGLFY	PFUFEN1	.PRO					
MGIOGLAKL	J	ADVAPSA	I	REND	IKSYFGRKVA	IDASMS	IYQFL	I	AVRQ	--GGDVLQNEEGETT	SHLMGMFY	HUMFEN1	.PRO				
MGIHGLAKL	J	ADVAPSA	I	REND	IKSYFGRKVA	IDASMS	IYQFL	I	AVRQ	--GGDVLQNEEGETT	S-LMGMFY	MUSFEN1	.PRO				
MGIKGLNA	I	SEHVPSA	I	RKSD	IKSFFGRKVA	IDASMS	IYQFL	I	AVROODGGQLTNEAGETT	SHLMGMFY	YST510	.PRO					
MGVHSFWD	IAG	----	PTARPVR	LESLEDKRM	AVDASI	WIYQFL	KAVRDOEGNA	VKN	----	SHITGFFR	YSTRAD2	.PRO					
MGVSGLWN	I	----	PVKRPVK	LETLVNKR	LAIDAS	WIYQFL	KAVRDK	EGNOLKS	----	SHVVGFFR	SPORAD13	.PRO					
MGVOGLWKLE	----	CSGRQVS	PEALEGK	I	LAVD	I	SIWLNQAL	KGYRDRH	GN	SIEN	----	PHLLTLFH	HUMXPG	.PRO			
MGVOGLWKLE	----	CSGHRVS	PEALEGK	V	LAVD	I	SIWLNQAL	KGYRDSH	GN	V	SIEN	----	AHLLTLFH	MUSXPG	.PRO		
MGVOGLWKLE	----	CSGRP	INPGT	LEGK	I	LAVD	I	SIWLNQAV	KGARDRO	GN	AI	ON	----	AHLLTLFH	XENXPG	.PRO	
MT	INGI	WEWANHVV	----	RKVPNET	MROK	TLS	IDGHI	WL	YESLKGCEAH	HOOT	----	----	PNSYL	VTFFT	CEL	RAD2	.PRO

	80	90	100	110	120	130	140
4	KTIHLENDITPIWVFDGEP	PKLKEKTRKVRRE	MKEKAELKMK	EAIKK----	EDFEEAAKYAKR	VSYLTP	MJAFEN1.PRO
4	RTINLMEAGIKP	VYVFDGEPPEFK	KELEKRREAREE	AEEKWREALEK----	GEIEEAR	KYAQRATRVNE	PFUFEN1.PRO
0	RTIRMMENGIKP	VYVFDGKPPOLK	SGELAKRSERRAE	AEKOLQAAQAA----	GAEQ	VEKFTKRLVKVTK	HUMFEN1.PRO
9	RTIRM-ENG	IKP	VYVFDGKPPOLK	SGELAKRSERRAE	AEKOLQAAQEA----	GMEEEVEKFTKRLVKVTK	MUSFEN1.PRO
1	RTL	MIDNGIKPCYV	FDGKPPDLK	SHELTKRSSRRVET	EKKLA--EA----	TTELEKMKOERRLVK	VSKYST510.PRO
1	RICKLLYFGIRP	VFDGGVPVLK	RETIRQKERROQK	RESAKSTARKLLALOLONGS	NDNKRDSD	DEVTM	YSTRAD2.PRO
1	RICKLLFFG	IKPVFVFDGGAP	SLKROTIOKROARRLO	REENATVTANKLLALOMRHO	AMLLKRDAD	EVTO	SPORAD13.PRO
1	RLCKLLFFRIRP	IFVFDGOAPLLK	QOTLVKRRORKOL	ASSDSRKTTEKLLK	TFLKROAIKTERIA	AATVTG	HUMXPG.PRO
1	RLCKLLFFRIRP	IFVFDGDAPLLK	KOTLAKRRORKDSAS	IOSRKTTEKLLK	TFLKROALKTDRI	AASVTG	MUSXPG.PRO
1	RLCKLLFFRIRP	IFVFDGEAPLLK	ROTLAKRRORTDKAS	NOARKTNEKLLRT	FCLKROAIKAERIA	AATVTG	XENXPG.PRO
0	RIQRLLLELK	IPIVVF	DNINASSSAHESKD	QNEFVPRKRRSFGD	SPFTNLV-----	CELRA	D2.PRO

**FIGURE 70-B**

	150	160	170	180	190	200	210
130	KMVENCKYLLSLMGIPYVEAPSEGEAQASVMAKKGQVWAVVSQOYDALLYGAPRVVRNLTTTKEM----	MJAFEN1.PRO					
130	MLJEDAKKLLLELMGIPYVOAPSEGEAQAAAYMAAKGVSVASQDYDSLFLGAPRLVRNLTTITGKRKLPGK	PFUFEN1.PRO					
136	QHNOECKHLLSLMGIPYLDAPSEAEASCAALVKAGKVYAAATEDMDCLTFGSPVLMRHLTASEAKKLPIQ	HUMFEN1.PRO					
134	QHNOECKHLLSLMGIPYLDAPSEAEASCAALAKAGKVYAAATEDMDCLTFGSPVLMRHLTASEAKKLPIQ	MUSFEN1.PRO					
134	EHNEEAOKLLGLMGIPYIIAPTEAEAOCAELAKKGKVYAAASEMDTLCYRTPFLLRHLTFSEAKKEPIH	YST510.PRO					
131	OMIKEVQELLSRFGIPYJITAPMEAEAOCAELLQNLVDGIITDQSOVFLFGGTKIYKNMFHEKNY----	YSTRAD2.PRO					
131	VMIKECQELLRLFGLPYIVAPQEAEOQCSKELLEKLVDGIVTDQSDVFLFGGTRVYRNMFNONKF----	SPORAD13.PRO					
131	QMFLESQELLRLFGIPYIQAPMEAEAOCAIILDLTDQTSGTITQOOSDIWLFGARHVYRNFNKNKF----	HUMXPG.PRO					
131	QMFLESQELLRLFGVPYIQAPMEAEAOCAVLDLSDQTSGTITDQSDIWLFGARHVYKNFFNKNKF----	MUSXPG.PRO					
131	QMCLESQELLQLFGIPYIVAPMEAEAOCAIILDLTDQTSGTITDQSDIWLFGARHVYKNFFSQNHK----	XENXPG.PRO					
111	DHVVYKTNALLTELGIKVIIPAGGOEAOCCARLEDLGVTSGCITTDFOYFLFGGKNLYRFDFTAGT-----	CELRAD2.PRO					

	220	230	240	250	260	270	280
195	-----	PELIELNEVLEDRLISLODLIDIAIFMGTDYNPGGV--K--GIGFKRAYELVRSGVAK--DV					MJAFEN1.PRO
200		NYVE-1KPELILEEVKELKLTREKLIELAILVGTDYNPGG[-K--GIGLKKALEIVRHSKDPLAKF					PFUFEN1.PRO
206		EFHLSRJLQELGLNOEQVOLCILLGSDYCESIRGIGPKRAVDLIQK--HKSIEEIVRRLOPN----					KY HUFEN1.PRO
204		EFHLSRVLQELGLNOEQVOLCILLGSDYCESIRGIGAKRAVDLIQK--HKSIEEIVRRLOPS----					KY MUSFEN1.PRO
204		EIDTELVLRGLOLTIEQFVOLCIMLGCDYCESIRGVGPVTALKLJKT--HGSIEKIVEFIESGESNNTKW					YST510.PRO
198		FYDAESILKLLGLDRKNMIELAQLLGSDYTNGLKGMGPVSSIEVJAEF--GNLKNFKDWNNGOFOKRK					YSTRAD2.PRO
198		LYLMDDMKREFNVNOMDLIKLAHLLGSDYTMGLSRVGPVLAELILHEFPDGTGLFEFKKWFQRLSTGHAS					SPORAD13.PRO
198		YYQYVDFHNLGLDRNKLINLAYLLGSDYTEGIP TVGCVTAMEILNEFPGHGLEPLLKFSEWWHEAQKNP					HUMXPG.PRO
198		YYQYVDFYSOLGLDRNKLINLAYLLGSDYTEGIP TVGCVTAMEILNEFPGRGLDPLLKFSEWWHEAQNNK					MUSXPG.PRO
198		YYOYADFHNLGLDRSKLINLAYLLGSDYTEGIP TVGYVVSAMEILNEFPGOGLEPLVKFEWWSEAOXDK					XENXPG.PRO
175	-----	-----	-----	-----	SSTACLHDIMHLSLGRMF-----	-----	CELRAD2.PRO





FIGURE 70-E

22 DAWFKZ  
35 ESWFKR  
75 KFKRGK  
73 KFRRGK  
77 VTKGRR  
90 ---RKM  
83 SKRRRK  
46 RKRK TZ  
38 RRKKKT  
23 TVKRK  
29 ELGDSD

MJAFEN1.PRO  
PFUFEN1.PRO  
HUMFEN1.PRO  
MUSFEN1.PRO  
YST510.PRO  
YSTRAD2.PRO  
SPORAD13.PRO  
HUMXPG.PRO  
MUSXPG.PRO  
XENXPG.PRO  
CELRAD2.PRO

FIGURE 71

